

STIC-Biotech/ChemLib

168083

From: Switzer, Juliet
Sent: Thursday, October 06, 2005 4:20 PM
To: STIC-Biotech/ChemLib
Subject: us 10/798678

please search:

seq id no 7
seq id no 8
seq id no 9
seq id no 10
seq id no 11
seq id no 12
seq id 1,
seq id 2,

in prior art nucleic acid databases
please return results on disk.

THANKS

Juliet Switzer
Art Unit 1634
phone: 571-272-0753
office: Remsen 2A61
mailbox: 2C70

RECEIVED
OCT - 6 2005
STIC/CHEM. DIVISION
(STIC)

Searcher: Jan
Searcher Phone: 122504
Date Searcher Picked up: 10/14/05
Date completed: 10/14/05
Searcher Prep Time: 10
Online Time: 15

Type of Search
NA# ✓ AA#: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: ✓
WWW/Internet: _____
Other (Specify): _____

(FILE 'HOME' ENTERED AT 15:12:53 ON 24 OCT 2005)

FILE 'MEDLINE, BIOSIS, CAPLUS' ENTERED AT 15:13:11 ON 24 OCT 2005

FILE 'AGRICOLA, FROSTI, MEDLINE, BIOSIS, CAPLUS' ENTERED AT 15:13:21 ON 24 OCT 2005

L1 2918 SEA PLU=ON (CKM OR (CREATINE(3A) KINASE(3A) MUSCLE(3A) GENE))
L2 17 SEA PLU=ON L1 AND (PIG OR PORCINE OR SUS OR SCROFA OR BOAR OR PORK)
L3 9 DUP REM L2 (8 DUPLICATES REMOVED)
D TI 1-9
D IBIB AB 5 2

FILE 'STNGUIDE' ENTERED AT 15:15:49 ON 24 OCT 2005

FILE 'MEDLINE, BIOSIS, CAPLUS' ENTERED AT 15:16:21 ON 24 OCT 2005
D KWIC 5

FILE 'STNGUIDE' ENTERED AT 15:16:22 ON 24 OCT 2005

L4 0 SEA PLU=ON L1 AND (MEAT OR GROWTH OR PH OR MINOLTA OR DRIP OR FIRM OR WEIGHT OR GAIN)

FILE 'AGRICOLA, FROSTI, MEDLINE, BIOSIS, CAPLUS' ENTERED AT 15:22:53 ON 24 OCT 2005

L5 172 SEA PLU=ON L4
L6 125 DUP REM L5 (47 DUPLICATES REMOVED)
D TI L6
L7 18 SEA PLU=ON L6 AND L1/TI
D TI 1-18
D IBIB AB 6
D IBIB AB 7
L8 78 SEA PLU=ON L6 AND L1/AB
L9 66 SEA PLU=ON L8 NOT L7
D TI 1-66
D IBIB AB 39

FILE 'STNGUIDE' ENTERED AT 15:31:35 ON 24 OCT 2005

FILE 'MEDLINE, BIOSIS, CAPLUS' ENTERED AT 15:33:16 ON 24 OCT 2005
D IBIB AB 12

FILE 'STNGUIDE' ENTERED AT 15:33:16 ON 24 OCT 2005

FILE 'AGRICOLA, FROSTI, MEDLINE, BIOSIS, CAPLUS' ENTERED AT 15:38:08 ON 24 OCT 2005

L10 57 SEA PLU=ON L1 AND (SNP OR POLYMORPH? OR MARKER OF ALLELE)
L11 52 SEA PLU=ON L10 NOT (L9 OR L3 OR L7)
L12 32 DUP REM L11 (20 DUPLICATES REMOVED)
D TI 1-32

FILE 'STNGUIDE' ENTERED AT 15:41:16 ON 24 OCT 2005

FILE 'AGRICOLA, MEDLINE, BIOSIS, CAPLUS' ENTERED AT 15:43:42 ON 24 OCT 2005
D IBIB AB 1 2 3 10

FILE 'STNGUIDE' ENTERED AT 15:43:43 ON 24 OCT 2005

FILE 'STNGUIDE' ENTERED AT 15:43:48 ON 24 OCT 2005

FILE 'AGRICOLA, MEDLINE, BIOSIS, CAPLUS' ENTERED AT 15:56:43 ON 24 OCT 2005
D IBIB AB 30 28 27

FILE 'STNGUIDE' ENTERED AT 15:56:43 ON 24 OCT 2005

FILE 'AGRICOLA, MEDLINE, BIOSIS, CAPLUS' ENTERED AT 15:59:15 ON 24 OCT

2005

D IBIB AB 31 32

FILE 'STNGUIDE' ENTERED AT 15:59:15 ON 24 OCT 2005

L13 0 SEA PLU=ON L1 OR CKMM

FILE 'AGRICOLA, FROSTI, MEDLINE, BIOSIS, CAPLUS' ENTERED AT 16:00:00 ON
24 OCT 2005

L14 3024 SEA PLU=ON L13

L15 0 SEA PLU=ON L14 AND MYTONIC

L16 73 SEA PLU=ON L14 AND MYOTONIC

L17 39 SEA PLU=ON L16 AND (RFLP OR NCO1 OR POLYMORPH? OR SNP OR
ALLEL? OR VARIAN?)

L18 23 DUP REM L17 (16 DUPLICATES REMOVED)

D TI 1-23

D IBIB AB 3

D IBIB AB 17

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OM nucleic - nucleic search, using sw model

Run on: October 11, 2005, 06:09:23 ; Search time 17.7647 Seconds
(without alignments)
6664.609 Million cell updates/sec

Title: US-10-798-678-7
Perfect score: 20
Sequence: 1 cagcccatacaaggccatgg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	ID		Description
1	20	100.0	20	13	ADS13178		Ads13178 PCR prime
2	20	100.0	236	13	ADS13172		Ads13172 Porcine c
3	20	100.0	365	6	ABK82051		Abk82051 Mouse mus
4	20	100.0	365	6	AAL44606		Aal44606 Murine mu

	5	20	100.0	366	6	AAL44622	Aal44622 Rat muscl
	6	20	100.0	377	6	AAL44614	Aal44614 Human mus
	7	20	100.0	576	6	AAL44602	Aal44602 Murine MC
	8	20	100.0	594	6	ABK82019	Abk82019 Creatine
	9	20	100.0	655	8	ABZ20800	Abz20800 Murine MC
	10	20	100.0	951	6	ABK82050	Abk82050 Mouse mus
	11	20	100.0	951	6	AAL44605	Aal44605 Murine mu
	12	20	100.0	955	6	AAD37254	Aad37254 Adeno-ass
	13	20	100.0	1121	6	AAL44603	Aal44603 Murine MC
	14	20	100.0	1263	6	AAL44604	Aal44604 Murine MC
	15	20	100.0	1361	2	AAT61698	Aat61698 Mouse mus
	16	20	100.0	1682	6	AAL44616	Aal44616 Rat muscl
	17	20	100.0	2903	6	AAL44608	Aal44608 Human mus
	18	20	100.0	3357	6	AAL44595	Aal44595 Murine mu
	19	20	100.0	3364	2	AAV07266	Aav07266 Muscle cr
	20	20	100.0	4101	8	ACC47993	Acc47993 Mouse mus
	21	20	100.0	4414	6	AAD37260	Aad37260 Adeno-ass
	22	20	100.0	4476	6	AAD37259	Aad37259 Adeno-ass
	23	20	100.0	4498	6	AAD37258	Aad37258 Adeno-ass
	24	20	100.0	4825	6	AAD37257	Aad37257 Adeno-ass
	25	20	100.0	4966	6	AAD37256	Aad37256 Adeno-ass
	26	20	100.0	5149	6	AAD37255	Aad37255 Adeno-ass
	27	17.4	87.0	96596	9	ADA02504	Ada02504 Human BAC
	28	17.4	87.0	96596	10	ADB72242	Adb72242 Human BAC
	29	17.4	87.0	96596	10	ADE95752	Ade95752 Human BAC
c	30	16.8	84.0	1362	8	ACA53986	Aca53986 Prokaryot
	31	16.8	84.0	2902	6	ABI99326	Abi99326 Mouse isc
	32	16.8	84.0	2902	12	ADJ75755	Adj75755 Marker ge
	33	16.8	84.0	19062	3	AAF21280	Aaf21280 Human low
	34	16.8	84.0	19062	10	ABZ96974	Abz96974 Human nuc
	35	16.8	84.0	19062	11	ABD20823	Abd20823 Human pul
	36	16.8	84.0	23142	3	AAA35158	Aaa35158 Human ade
	37	16.8	84.0	30417	3	AAA35160	Aaa35160 Human ade
	38	16.8	84.0	30417	3	AAF21282	Aaf21282 Human low
	39	16.8	84.0	30417	10	ABZ96976	Abz96976 Human nuc
	40	16.8	84.0	30417	11	ABD20825	Abd20825 Human pul
c	41	16.8	84.0	49965	11	ACN44460	Acn44460 Mouse gen
	42	16.8	84.0	88191	8	ABX14763	Abx14763 Genomic D
c	43	16.8	84.0	101209	11	ACN44154	Acn44154 Human gen
	44	16.4	82.0	303	12	ACH83321	Ach83321 Human gen
	45	16.4	82.0	597	12	ACH69621	Ach69621 Human gen

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OM nucleic - nucleic search, using sw model

Run on: October 11, 2005, 06:09:25 ; Search time 5.4902 Seconds
(without alignments)
5960.722 Million cell updates/sec

Title: US-10-798-678-7
Perfect score: 20
Sequence: 1 cagcccatatacaaggccatgg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	20	100.0	1361	1	US-08-530-529-1	Sequence 1, Appli
2	20	100.0	1361	3	US-09-119-264-1	Sequence 1, Appli
3	20	100.0	3364	2	US-08-735-609-9	Sequence 9, Appli
4	20	100.0	3364	2	US-08-735-609-9	Sequence 9, Appli
5	20	100.0	3364	3	US-09-315-372-9	Sequence 9, Appli
6	20	100.0	3364	3	US-09-244-752-9	Sequence 9, Appli
7	20	100.0	3364	3	US-09-245-497-9	Sequence 9, Appli
8	20	100.0	3364	3	US-09-562-919-9	Sequence 9, Appli
9	17.4	87.0	374159	4	US-09-949-016-15868	Sequence 15868, A
10	16.8	84.0	9391	4	US-09-949-016-14299	Sequence 14299, A
11	16.8	84.0	10103	2	US-08-457-273B-7	Sequence 7, Appli

	12	16.4	82.0	36611	4	US-09-949-016-17287	Sequence 17287, A
	13	15.8	79.0	601	4	US-09-949-016-84943	Sequence 84943, A
	14	15.8	79.0	601	4	US-09-949-016-204750	Sequence 204750,
c	15	15.8	79.0	931	4	US-09-270-767-13966	Sequence 13966, A
	16	15.8	79.0	5172	4	US-09-949-016-5785	Sequence 5785, Ap
	17	15.8	79.0	7890	4	US-09-949-016-2425	Sequence 2425, Ap
	18	15.8	79.0	9997	1	US-08-246-982A-15	Sequence 15, Appl
	19	15.8	79.0	9997	1	US-08-453-265-15	Sequence 15, Appl
c	20	15.8	79.0	32327	4	US-09-949-016-14108	Sequence 14108, A
c	21	15.8	79.0	35100	2	US-08-770-379-18	Sequence 18, Appl
c	22	15.8	79.0	35100	3	US-08-757-669A-18	Sequence 18, Appl
c	23	15.8	79.0	35100	3	US-09-230-371A-18	Sequence 18, Appl
	24	15.8	79.0	51719	4	US-09-918-686-2	Sequence 2, Appli
	25	15.8	79.0	53769	4	US-09-949-016-17527	Sequence 17527, A
	26	15.8	79.0	92139	4	US-09-918-686-1	Sequence 1, Appli
	27	15.8	79.0	93398	4	US-09-949-016-14167	Sequence 14167, A
	28	15.4	77.0	303	3	US-08-867-902F-2	Sequence 2, Appli
	29	15.4	77.0	585	3	US-08-867-902F-3	Sequence 3, Appli
	30	15.4	77.0	882	4	US-09-949-016-2156	Sequence 2156, Ap
c	31	15.4	77.0	1540	4	US-09-560-761B-3	Sequence 3, Appli
c	32	15.4	77.0	1618	4	US-09-560-761B-15	Sequence 15, Appl
	33	15.4	77.0	6560	4	US-09-949-016-16878	Sequence 16878, A
	34	15.4	77.0	7424	4	US-09-949-016-13898	Sequence 13898, A
c	35	15.4	77.0	59240	4	US-09-949-016-11933	Sequence 11933, A
c	36	15.2	76.0	25	4	US-09-396-196G-104630	Sequence 104630,
c	37	15.2	76.0	56	1	US-08-211-202-55	Sequence 55, Appl
	38	15.2	76.0	381	4	US-09-949-016-3356	Sequence 3356, Ap
c	39	15.2	76.0	601	4	US-09-949-016-23103	Sequence 23103, A
c	40	15.2	76.0	601	4	US-09-949-016-23104	Sequence 23104, A
c	41	15.2	76.0	601	4	US-09-949-016-81227	Sequence 81227, A
c	42	15.2	76.0	601	4	US-09-949-016-81228	Sequence 81228, A
	43	15.2	76.0	601	4	US-09-949-016-120914	Sequence 120914,
	44	15.2	76.0	601	4	US-09-949-016-120915	Sequence 120915,
c	45	15.2	76.0	601	4	US-09-949-016-126330	Sequence 126330,

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OM nucleic - nucleic search, using sw model

Run on: October 11, 2005, 06:09:25 ; Search time 57.5948 Seconds
(without alignments)
2418.567 Million cell updates/sec

Title: US-10-798-678-7
Perfect score: 20
Sequence: 1 cagcccatacaaggccatgg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 8443130 seqs, 3482420727 residues

Total number of hits satisfying chosen parameters: 16886260

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq:*
21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:*
22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	20	100.0	20	20	20	US-10-798-678-7	Sequence 7, Appli
2	20	100.0	236	20	20	US-10-798-678-1	Sequence 1, Appli
3	20	100.0	365	17	17	US-10-149-736-93	Sequence 93, Appl
4	20	100.0	365	21	21	US-10-964-536-93	Sequence 93, Appl
5	20	100.0	591	17	17	US-10-149-736-61	Sequence 61, Appl
6	20	100.0	591	21	21	US-10-964-536-61	Sequence 61, Appl
7	20	100.0	655	15	15	US-10-156-604-18	Sequence 18, Appl
8	20	100.0	951	17	17	US-10-149-736-92	Sequence 92, Appl
9	20	100.0	951	21	21	US-10-964-536-92	Sequence 92, Appl
10	20	100.0	955	10	10	US-09-845-416-26	Sequence 26, Appl
11	20	100.0	4101	21	21	US-10-492-901-8	Sequence 8, Appli
12	20	100.0	4414	10	10	US-09-845-416-32	Sequence 32, Appl
13	20	100.0	4476	10	10	US-09-845-416-31	Sequence 31, Appl
14	20	100.0	4498	10	10	US-09-845-416-30	Sequence 30, Appl
15	20	100.0	4825	10	10	US-09-845-416-29	Sequence 29, Appl
16	20	100.0	4966	10	10	US-09-845-416-28	Sequence 28, Appl
17	20	100.0	5149	10	10	US-09-845-416-27	Sequence 27, Appl
18	17.4	87.0	96596	18	18	US-10-052-482-10	Sequence 10, Appl
c 19	16.8	84.0	1362	17	17	US-10-282-122A-41856	Sequence 41856, A
20	16.8	84.0	2902	22	22	US-10-631-467-1007	Sequence 1007, Ap
c 21	16.8	84.0	49965	13	13	US-10-087-192-919	Sequence 919, App
c 22	16.8	84.0	70931	19	19	US-10-331-053-67	Sequence 67, Appl
23	16.8	84.0	88191	9	9	US-09-799-799-3	Sequence 3, Appli
c 24	16.8	84.0	101209	13	13	US-10-087-192-460	Sequence 460, App
25	16.4	82.0	303	16	16	US-10-029-386-16516	Sequence 16516, A
26	16.4	82.0	488	22	22	US-10-972-079-48494	Sequence 48494, A
27	16.4	82.0	597	16	16	US-10-029-386-2816	Sequence 2816, Ap
28	16.4	82.0	731	20	20	US-10-425-115-34966	Sequence 34966, A
c 29	16	80.0	520	13	13	US-10-027-632-220401	Sequence 220401,
c 30	16	80.0	520	17	17	US-10-027-632-220401	Sequence 220401,
31	16	80.0	2779	17	17	US-10-369-493-27546	Sequence 27546, A
32	15.8	79.0	25	21	21	US-10-719-900-881425	Sequence 881425,
33	15.8	79.0	25	24	24	US-11-036-317-816437	Sequence 816437,
34	15.8	79.0	233	19	19	US-10-767-701-26021	Sequence 26021, A
c 35	15.8	79.0	264	18	18	US-10-424-599-105903	Sequence 105903,
c 36	15.8	79.0	281	18	18	US-10-424-599-27338	Sequence 27338, A
37	15.8	79.0	297	22	22	US-10-501-282-3433	Sequence 3433, Ap
38	15.8	79.0	362	22	22	US-10-756-149-4537	Sequence 4537, Ap
c 39	15.8	79.0	456	22	22	US-10-501-282-3437	Sequence 3437, Ap
c 40	15.8	79.0	600	22	22	US-10-972-079-7947	Sequence 7947, Ap
c 41	15.8	79.0	600	22	22	US-10-972-079-7948	Sequence 7948, Ap
c 42	15.8	79.0	600	22	22	US-10-972-079-26833	Sequence 26833, A
c 43	15.8	79.0	615	22	22	US-10-501-282-3435	Sequence 3435, Ap
44	15.8	79.0	711	19	19	US-10-767-701-7905	Sequence 7905, Ap
45	15.8	79.0	723	18	18	US-10-424-599-116237	Sequence 116237,

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OM nucleic - nucleic search, using sw model

Run on: October 11, 2005, 06:09:23 ; Search time 1133.57 Seconds
(without alignments)
10087.968 Million cell updates/sec

Title: US-10-798-678-1
Perfect score: 236
Sequence: 1 cagcccatacaaggccatgg.....ttccagcacagcccagccag 236

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%		Query			ID	Description
Result	No.	Score	Match	Length	DB			
c	1	151	64.0	173728	2	AC139878		AC139878 Sus scrof
c	2	134.8	57.1	155060	2	AC140158		AC140158 Felis cat
c	3	134.8	57.1	156383	2	AC135221		AC135221 Felis cat

c	4	133	56.4	197005	2	AC137535	AC137535 Bos tauru
c	5	130.8	55.4	163038	2	AC135542	AC135542 Pan trogl
c	6	130.2	55.2	188698	2	AC137531	AC137531 Papio anu
	7	127.6	54.1	2903	6	AX395377	AX395377 Sequence
	8	127.6	54.1	2903	9	HUMCKMM1	M21487 Human muscl
	9	127.6	54.1	160069	2	AC023329	AC023329 Homo sapi
	10	126	53.4	20454	9	AY585238	AY585238 Homo sapi
c	11	126	53.4	44052	9	AC005781	AC005781 Homo sapi
c	12	111	47.0	199160	2	AC137538	AC137538 Canis fam
	13	101.6	43.1	377	6	AX395383	AX395383 Sequence
	14	91.4	38.7	1682	6	AX395385	AX395385 Sequence
	15	91.4	38.7	1682	10	RATCKMUSCL	M27092 Rattus norv
c	16	91.4	38.7	201842	2	AC137646	AC137646 Rattus no
c	17	91.4	38.7	252619	2	AC095012	AC095012 Rattus no
c	18	91.4	38.7	260849	2	AC119447	AC119447 Rattus no
	19	89.2	37.8	591	6	AX538641	AX538641 Sequence
	20	87.8	37.2	1059	10	MUSCKM1	M13642 Mouse muscl
	21	87.8	37.2	4101	10	MUSMCKA	M21390 Mouse muscl
	22	86.2	36.5	166513	2	AC073787	AC073787 Mus muscu
c	23	86.2	36.5	196427	10	AC118017	AC118017 Mus muscu
c	24	86.2	36.5	316822	2	AC118016	AC118016 Mus muscu
	25	83.6	35.4	804	4	OCMCK1	X55146 Rabbit gene
	26	79.6	33.7	366	6	AX395391	AX395391 Sequence
	27	76.6	32.5	365	6	AX395375	AX395375 Sequence
	28	76.6	32.5	365	6	AX538673	AX538673 Sequence
	29	76.6	32.5	576	6	AX395371	AX395371 Sequence
	30	76.6	32.5	951	6	AX395374	AX395374 Sequence
	31	76.6	32.5	951	6	AX538672	AX538672 Sequence
	32	76.6	32.5	1121	6	AX395372	AX395372 Sequence
	33	76.6	32.5	1263	6	AX395373	AX395373 Sequence
	34	76.6	32.5	1361	6	AR024207	AR024207 Sequence
	35	76.6	32.5	1361	6	AR176159	AR176159 Sequence
	36	76.6	32.5	3357	6	AX395364	AX395364 Sequence
	37	76.6	32.5	3357	10	AF188002	AF188002 Mus muscu
	38	76.6	32.5	3364	6	AR091541	AR091541 Sequence
	39	76.6	32.5	3364	6	AR102234	AR102234 Sequence
	40	76.6	32.5	3364	6	AR230732	AR230732 Sequence
c	41	49.2	20.8	8147	6	AX345331	AX345331 Sequence
	42	44	18.6	87	6	AX395384	AX395384 Sequence
	43	42.6	18.1	8147	6	AX345330	AX345330 Sequence
c	44	42.6	18.1	59903	2	AC015782	AC015782 Homo sapi
c	45	39.8	16.9	42415	9	AC001644	AC001644 Genomic s

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OM nucleic - nucleic search, using sw model

Run on: October 11, 2005, 06:09:23 ; Search time 8436.1 Seconds
(without alignments)
5030.955 Million cell updates/sec

Title: US-10-798-678-2
Perfect score: 1115
Sequence: 1 tccatctggcttcaccctgg.....catccctgccaggtcacccc 1115

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	150.4	13.5	565	9	CL409209	CL409209 RPCI44_41
	2	143.6	12.9	651	6	CB469586	CB469586 sn09_D11.
c	3	143	12.8	310	2	BF703913	BF703913 MI-P-A3-a
c	4	141	12.6	518	6	CA780218	CA780218 MPL384_4
c	5	139.4	12.5	508	9	CL332968	CL332968 CH242_12B
	6	139.2	12.5	790	6	CB169406	CB169406 KYE602702
c	7	135	12.1	680	5	BP435256	BP435256 BP435256
	8	132.8	11.9	319	7	CO988373	CO988373 UMC-pd3en
	9	132.8	11.9	499	5	BQ600069	BQ600069 MI-P-E7-a

	10	132	11.8	355	7	CV101131	CV101131 UMC-pcryb
	11	131.6	11.8	521	9	CL377300	CL377300 RPCI44_44
	12	131.6	11.8	608	9	CL343481	CL343481 RPCI44_27
c	13	131.2	11.8	395	9	CL324716	CL324716 RPCI44_47
c	14	131	11.7	822	5	BP163337	BP163337 BP163337
	15	130.8	11.7	637	9	CL345127	CL345127 RPCI44_27
	16	129.6	11.6	452	2	BE014850	BE014850 126725 MA
c	17	129.6	11.6	647	9	CL349292	CL349292 RPCI44_30
c	18	129.2	11.6	574	9	CL370833	CL370833 RPCI44_30
c	19	129.2	11.6	616	9	CL379887	CL379887 RPCI44_42
c	20	129.2	11.6	791	5	BP165521	BP165521 BP165521
c	21	129	11.6	640	9	CL384715	CL384715 RPCI44_32
	22	128.6	11.5	536	5	BQ601693	BQ601693 MI-P-HO-a
	23	128.6	11.5	615	5	BX671723	BX671723 BX671723
	24	128.6	11.5	624	5	BX671722	BX671722 BX671722
c	25	127.8	11.5	634	7	CF358983	CF358983 818546 MA
	26	127.6	11.4	521	4	BG732502	BG732502 333235 MA
	27	127.6	11.4	624	9	CL343089	CL343089 RPCI44_27
	28	127.6	11.4	695	9	CL343079	CL343079 RPCI44_27
c	29	127.4	11.4	605	9	CL334843	CL334843 RPCI44_25
c	30	127.4	11.4	742	5	BP437890	BP437890 BP437890
c	31	127	11.4	383	7	CO939300	CO939300 UMC-pd20f
c	32	127	11.4	624	9	CL367182	CL367182 RPCI44_36
	33	126.8	11.4	644	9	CL322088	CL322088 RPCI44_39
c	34	126.8	11.4	706	5	BP444141	BP444141 BP444141
	35	126.6	11.4	619	4	BI181906	BI181906 UNL-P-FN-
	36	126.2	11.3	578	5	BP159539	BP159539 BP159539
c	37	126	11.3	375	7	CO953840	CO953840 UMC-pnata
c	38	126	11.3	813	7	CK465695	CK465695 936829 MA
	39	125.8	11.3	501	9	CL365674	CL365674 RPCI44_35
	40	125.6	11.3	511	9	CL383879	CL383879 RPCI44_32
c	41	125.6	11.3	587	9	CL379777	CL379777 RPCI44_42
	42	125.4	11.2	522	2	BF075098	BF075098 223882 MA
c	43	125.2	11.2	721	9	CL330422	CL330422 CH242_3F4
c	44	125	11.2	411	9	CL322335	CL322335 RPCI44_40
	45	125	11.2	601	9	CL387400	CL387400 RPCI44_28

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OM nucleic - nucleic search, using sw model

Run on: October 11, 2005, 06:09:25 ; Search time 3210.91 Seconds
(without alignments)
2418.567 Million cell updates/sec

Title: US-10-798-678-2
Perfect score: 1115
Sequence: 1 tccatctggcttcaccctgg.....catccctgccaggtcacccc 1115

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 8443130 seqs, 3482420727 residues

Total number of hits satisfying chosen parameters: 16886260

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:*
- 22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				Description
	No.	Score	Match	Length	DB	ID	
	1	1115	100.0	1115	20	US-10-798-678-2	Sequence 2, Appli
	2	129.6	11.6	27750	20	US-10-451-503A-4	Sequence 4, Appli
	3	122.4	11.0	30535	20	US-10-451-503A-7	Sequence 7, Appli
c	4	121.6	10.9	1149	19	US-10-471-220-12	Sequence 12, Appl
	5	121.6	10.9	1150	21	US-10-481-160-7	Sequence 7, Appli
c	6	101.2	9.1	4629	20	US-10-475-757-23	Sequence 23, Appl
	7	100.2	9.0	396	17	US-10-113-664A-116	Sequence 116, App
	8	98.4	8.8	11864	20	US-10-451-503A-6	Sequence 6, Appli
c	9	96.8	8.7	30535	20	US-10-451-503A-7	Sequence 7, Appli
	10	93.8	8.4	778	16	US-10-257-826A-202	Sequence 202, App
	11	91.2	8.2	26642	20	US-10-451-503A-2	Sequence 2, Appli
c	12	90.4	8.1	9098	22	US-10-503-464-1	Sequence 1, Appli
c	13	90	8.1	480	19	US-10-471-220-7	Sequence 7, Appli
c	14	89.2	8.0	3789	20	US-10-475-757-22	Sequence 22, Appl
	15	87.8	7.9	15572	21	US-10-499-406-3	Sequence 3, Appli
	16	87.2	7.8	9339	20	US-10-451-503A-8	Sequence 8, Appli
c	17	87.2	7.8	13370	20	US-10-451-503A-3	Sequence 3, Appli
	18	84.2	7.6	726	16	US-10-257-826A-207	Sequence 207, App
	19	83.8	7.5	1095	10	US-09-950-022-11	Sequence 11, Appl
	20	83.8	7.5	1095	24	US-11-075-134-11	Sequence 11, Appl
	21	83.2	7.5	1224	21	US-10-481-160-4	Sequence 4, Appli
	22	83.2	7.5	1938	17	US-10-125-994A-3	Sequence 3, Appli
	23	83.2	7.5	8989	17	US-10-125-994A-8	Sequence 8, Appli
c	24	82.4	7.4	15572	21	US-10-499-406-3	Sequence 3, Appli
	25	81.8	7.3	500	17	US-10-125-994A-16	Sequence 16, Appl
	26	81.8	7.3	13370	20	US-10-451-503A-3	Sequence 3, Appli
c	27	81.2	7.3	1095	17	US-10-294-191A-12	Sequence 12, Appl
	28	81	7.3	760	16	US-10-257-826A-200	Sequence 200, App
c	29	80.8	7.2	719	16	US-10-257-826A-204	Sequence 204, App
c	30	80.8	7.2	994	19	US-10-679-064-34	Sequence 34, Appl
	31	79.6	7.1	406	17	US-10-113-664A-115	Sequence 115, App
c	32	79.6	7.1	1205	19	US-10-679-064-30	Sequence 30, Appl
	33	78.8	7.1	4411	20	US-10-451-503A-5	Sequence 5, Appli
c	34	78.2	7.0	27750	20	US-10-451-503A-4	Sequence 4, Appli
c	35	75.8	6.8	525	20	US-10-798-678-6	Sequence 6, Appli
c	36	75.8	6.8	11864	20	US-10-451-503A-6	Sequence 6, Appli
c	37	74.6	6.7	8980	21	US-10-499-406-1	Sequence 1, Appli
	38	73.8	6.6	2685	17	US-10-125-994A-10	Sequence 10, Appl
	39	72	6.5	310	17	US-10-113-664A-104	Sequence 104, App
c	40	71.2	6.4	13116	21	US-10-499-406-2	Sequence 2, Appli
	41	70.6	6.3	4023	18	US-10-398-666-11	Sequence 11, Appl
c	42	70.4	6.3	288	17	US-10-113-664A-11	Sequence 11, Appl
c	43	70.4	6.3	789	16	US-10-257-826A-199	Sequence 199, App
c	44	69.8	6.3	5662	19	US-10-679-064-28	Sequence 28, Appl
	45	69.4	6.2	5662	19	US-10-679-064-28	Sequence 28, Appl

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OM nucleic - nucleic search, using sw model

Run on: October 11, 2005, 06:09:25 ; Search time 306.078 Seconds
(without alignments)
5960.722 Million cell updates/sec

Title: US-10-798-678-2
Perfect score: 1115
Sequence: 1 tccatctggcttcaccctgg.....catccctgccaggtcacccc 1115

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%						Description
	No.	Score	Query Match	Length	DB	ID	
c	1	107.2	9.6	601	4	US-09-949-016-58443	Sequence 58443, A
	2	107.2	9.6	17353	4	US-09-949-016-13437	Sequence 13437, A
c	3	88.4	7.9	3588	1	US-08-197-792-32	Sequence 32, Appl
c	4	88.4	7.9	3588	1	US-08-459-850-32	Sequence 32, Appl
c	5	88.4	7.9	3588	1	US-08-459-214-32	Sequence 32, Appl
c	6	68.2	6.1	4267	3	US-08-949-155-51	Sequence 51, Appl
c	7	68.2	6.1	4267	3	US-09-819-964-51	Sequence 51, Appl
	8	67.2	6.0	1598	3	US-08-785-420-3	Sequence 3, Appli
c	9	66.8	6.0	1181	3	US-09-329-796-2	Sequence 2, Appli
c	10	63.4	5.7	291	3	US-09-329-796-1	Sequence 1, Appli
	11	59.4	5.3	4692	2	US-08-916-917-1	Sequence 1, Appli

	12	59.4	5.3	4692	2	US-08-972-631-1	Sequence 1, Appli
	13	59.4	5.3	4692	2	US-08-972-629-1	Sequence 1, Appli
	14	59.4	5.3	4692	2	US-08-972-630-1	Sequence 1, Appli
	15	59.4	5.3	4692	2	US-08-672-211-1	Sequence 1, Appli
	16	59.4	5.3	4692	3	US-09-225-170-1	Sequence 1, Appli
	17	56.6	5.1	4267	3	US-08-949-155-51	Sequence 51, Appl
	18	56.6	5.1	4267	3	US-09-819-964-51	Sequence 51, Appl
c	19	54.2	4.9	5917	3	US-08-692-922-1	Sequence 1, Appli
	20	50.4	4.5	3460	1	US-08-312-312A-1	Sequence 1, Appli
	21	48.8	4.4	1522	4	US-09-949-016-1695	Sequence 1695, Ap
	22	47.8	4.3	2343	2	US-09-018-760-3	Sequence 3, Appli
	23	47	4.2	5418	3	US-09-180-939-1	Sequence 1, Appli
	24	47	4.2	5418	4	US-09-462-740-1	Sequence 1, Appli
c	25	47	4.2	319608	4	US-09-539-333D-1	Sequence 1, Appli
c	26	47	4.2	319608	4	US-09-679-409-1	Sequence 1, Appli
c	27	44.2	4.0	3455	4	US-10-009-332-31	Sequence 31, Appl
	28	44	3.9	67181	4	US-09-949-016-13102	Sequence 13102, A
	29	43.2	3.9	7158	4	US-09-949-016-14106	Sequence 14106, A
c	30	43.2	3.9	19368	4	US-09-949-016-17548	Sequence 17548, A
	31	43.2	3.9	276237	4	US-09-949-016-17504	Sequence 17504, A
	32	42.8	3.8	601	4	US-09-949-016-65502	Sequence 65502, A
	33	42.8	3.8	601	4	US-09-949-016-65503	Sequence 65503, A
c	34	42.6	3.8	3462	4	US-10-009-332-30	Sequence 30, Appl
c	35	42.6	3.8	3467	4	US-10-009-332-25	Sequence 25, Appl
c	36	42.6	3.8	3469	4	US-10-009-332-27	Sequence 27, Appl
c	37	42.6	3.8	3470	4	US-10-009-332-28	Sequence 28, Appl
c	38	42.6	3.8	3473	4	US-10-009-332-24	Sequence 24, Appl
c	39	42.6	3.8	50368	4	US-09-949-016-13256	Sequence 13256, A
	40	42.4	3.8	601	4	US-09-949-016-56132	Sequence 56132, A
	41	42.4	3.8	70262	4	US-09-949-016-13375	Sequence 13375, A
	42	42.4	3.8	70263	4	US-09-949-016-12748	Sequence 12748, A
	43	42.2	3.8	601	4	US-09-949-016-120852	Sequence 120852,
c	44	42.2	3.8	44430	4	US-09-949-016-12468	Sequence 12468, A
c	45	42.2	3.8	44431	4	US-09-949-016-15882	Sequence 15882, A

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OM nucleic - nucleic search, using sw model

Run on: October 11, 2005, 06:09:23 ; Search time 990.382 Seconds
(without alignments)
6664.609 Million cell updates/sec

Title: US-10-798-678-2
Perfect score: 1115
Sequence: 1 tccatctggcttcaccctgg.....catccctgccaggtcacccc 1115

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1114.6	100.0	1115	13	ADS13173	Ads13173 Porcine c
2	126.4	11.3	3000	3	AAA65523	Aaa65523 Porcine B
c 3	121.6	10.9	1149	6	ABQ76894	Abq76894 PERV clon
4	121.6	10.9	1150	8	ABZ57867	Abz57867 Porcine e

c	5	114.6	10.3	4254	12	ADO80708	Ado80708 Porcine e
	6	105.6	9.5	2628	12	ADO80782	Ado80782 Porcine e
	7	104.2	9.3	6041	12	ADO80707	Ado80707 Porcine e
	8	104.2	9.3	6041	12	ADO80812	Ado80812 Porcine e
c	9	101.2	9.1	3790	8	AAD50838	Aad50838 Pig BAC 8
c	10	101.2	9.1	4590	8	AAD50839	Aad50839 Pig BAC 9
	11	100.2	9.0	396	8	ABZ37685	Abz37685 Porcine 5
	12	94.2	8.4	8480	2	AAZ27521	Aaz27521 Interleuk
c	13	94	8.4	600	3	AAA65439	Aaa65439 Porcine B
	14	93.8	8.4	778	6	AAS62076	Aas62076 Porcine m
c	15	90.4	8.1	8480	2	AAZ27521	Aaz27521 Interleuk
c	16	90.4	8.1	9098	10	ADD04783	Add04783 Pig RAG-1
c	17	90	8.1	480	6	ABQ76889	Abq76889 PERV clon
	18	88.8	8.0	3982	5	AAF27073	Aaf27073 Pig c-KIT
	19	88.8	8.0	3985	5	AAF27076	Aaf27076 Pig c-KIT
	20	88.8	8.0	3985	5	AAF27075	Aaf27075 Pig c-KIT
	21	88.8	8.0	3986	5	AAF27069	Aaf27069 Pig c-KIT
	22	88.8	8.0	3986	5	AAF27070	Aaf27070 Pig c-KIT
	23	88.8	8.0	3986	5	AAF27072	Aaf27072 Pig c-KIT
	24	88.8	8.0	3986	5	AAF27071	Aaf27071 Pig c-KIT
	25	88.8	8.0	4054	12	ADO80808	Ado80808 Porcine e
c	26	88.4	7.9	3588	1	AAN70317	Aan70317 Sequence
	27	88	7.9	11630	4	AAS02362	Aas02362 Galactosy
	28	88	7.9	27048	4	AAS02354	Aas02354 Porcine G
	29	87.8	7.9	4026	4	AAS02355	Aas02355 Porcine G
	30	87.8	7.9	15572	9	ACC85642	Acc85642 Mammalian
c	31	87.2	7.8	3235	12	ADO80700	Ado80700 Porcine e
	32	87.2	7.8	3986	5	AAF27067	Aaf27067 Pig c-KIT
	33	87.2	7.8	3986	5	AAF27074	Aaf27074 Pig c-KIT
	34	87.2	7.8	3986	5	AAF27066	Aaf27066 Pig c-KIT
	35	87.2	7.8	3986	5	AAF27068	Aaf27068 Pig c-KIT
	36	87.2	7.8	3986	12	ADP88010	Adp88010 Pig KIT g
c	37	87.2	7.8	5460	12	ADO80806	Ado80806 Porcine e
	38	87.2	7.8	8847	12	ADO25304	Ado25304 Porcine u
	39	86.6	7.8	550	12	ADO80769	Ado80769 Porcine e
c	40	86.2	7.7	1113	12	ADO80757	Ado80757 Porcine e
c	41	85.8	7.7	1384	12	ADO80743	Ado80743 Porcine e
c	42	85.8	7.7	2207	12	ADO80785	Ado80785 Porcine e
	43	85.6	7.7	4331	12	ADO80805	Ado80805 Porcine e
c	44	84.8	7.6	946	12	ADO80758	Ado80758 Porcine e
c	45	84.6	7.6	8053	10	ACF79694	Acf79694 Pig fibri

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OM nucleic - nucleic search, using sw model

Run on: October 11, 2005, 06:09:23 ; Search time 5355.64 Seconds
(without alignments)
10087.968 Million cell updates/sec

Title: US-10-798-678-2
Perfect score: 1115
Sequence: 1 tccatctggcttcaccctgg.....catccctgccaggtcacccc 1115

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query				ID	Description
			Match	Length	DB	%		
c	1	1016.2	91.1	173728	2	AC139878	AC139878	Sus scrof
	2	292.4	26.2	402	4	AF375765	AF375765	Sus scrof
	3	144	12.9	205338	2	AC141855	AC141855	Sus scrof

	4	143.2	12.8	164404	4	AC092874	AC092874	Sus	scrof
	5	140.8	12.6	152605	2	AC136886	AC136886	Sus	scrof
	6	140.8	12.6	161589	2	AC136881	AC136881	Sus	scrof
	7	139.2	12.5	200834	2	AC142092	AC142092	Sus	scrof
	8	138.8	12.4	201676	2	AC105367	AC105367	Sus	scrof
c	9	137.6	12.3	172407	2	AC148515	AC148515	Sus	scrof
c	10	137.6	12.3	175963	2	AC148913	AC148913	Sus	scrof
	11	136.6	12.3	152058	4	AC091756	AC091756	Sus	scrof
	12	136	12.2	184056	2	AC141857	AC141857	Sus	scrof
	13	134.6	12.1	144235	2	AC115534	AC115534	Sus	scrof
	14	134.6	12.1	162335	2	AC115535	AC115535	Sus	scrof
	15	134	12.0	164663	4	AC091402	AC091402	Sus	scrof
	16	133	11.9	184370	2	AC136887	AC136887	Sus	scrof
c	17	132.4	11.9	179378	2	AC127472	AC127472	Sus	scrof
c	18	131.8	11.8	167040	2	AC092194	AC092194	Sus	scrof
	19	131.8	11.8	194474	2	AC137536	AC137536	Sus	scrof
	20	131.4	11.8	190275	2	AC138042	AC138042	Sus	scrof
	21	131.4	11.8	191381	2	AC138046	AC138046	Sus	scrof
c	22	131.2	11.8	154101	2	AC136885	AC136885	Sus	scrof
	23	130.8	11.7	167171	2	AC139879	AC139879	Sus	scrof
	24	130.8	11.7	189985	2	AC140099	AC140099	Sus	scrof
	25	130.6	11.7	151588	2	AC105370	AC105370	Sus	scrof
c	26	130.6	11.7	184896	2	AC113229	AC113229	Sus	scrof
	27	130.2	11.7	114375	4	AB113357	AB113357	Sus	scrof
c	28	130.2	11.7	179691	4	BX296515	BX296515	Pig	DNA s
	29	130.2	11.7	204138	4	SSC427478	AJ427478	Sus	scrof
	30	129.6	11.6	27750	6	AX675819	AX675819	Sequence	
c	31	129.6	11.6	133877	2	AC138786	AC138786	Sus	scrof
	32	129.6	11.6	136646	2	AC135220	AC135220	Sus	scrof
	33	129.6	11.6	152549	2	AC133929	AC133929	Sus	scrof
	34	129.6	11.6	183431	2	AC138788	AC138788	Sus	scrof
	35	129.6	11.6	190191	2	AC138784	AC138784	Sus	scrof
	36	129.4	11.6	158735	2	AC104484	AC104484	Sus	scrof
c	37	129.2	11.6	121937	2	AC146934	AC146934	Sus	scrof
c	38	129.2	11.6	150305	4	AC087423	AC087423	Sus	scrof
c	39	129	11.6	102386	4	AC091404	AC091404	Sus	scrof
c	40	128.8	11.6	135508	2	AC120215	AC120215	Sus	scrof
c	41	128.8	11.6	151453	2	AC118988	AC118988	Sus	scrof
	42	128.8	11.6	152577	2	AC148863	AC148863	Sus	scrof
	43	128.8	11.6	165036	2	AC120214	AC120214	Sus	scrof
c	44	128.8	11.6	165619	2	AC145444	AC145444	Sus	scrof
c	45	128.8	11.6	169208	2	AC130791	AC130791	Sus	scrof

OM nucleic - nucleic search, using sw model

Run on: October 11, 2005, 06:09:23 ; Search time 1785.58 Seconds
 (without alignments)
 5030.955 Million cell updates/sec

Title: US-10-798-678-1
 Perfect score: 236
 Sequence: 1 cagcccatacaaggccatgg.....ttccagcacagcccagccag 236

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : EST:*
 1: gb_est1:*
 2: gb_est2:*
 3: gb_htc:*
 4: gb_est3:*
 5: gb_est4:*
 6: gb_est5:*
 7: gb_est6:*
 8: gb_gss1:*
 9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	85	36.0	817	5	BP171166 BP171166
2	60.4	25.6	583	5	BP231401 BP231401
3	58	24.6	701	5	BP439864 BP439864
4	46	19.5	560	5	BP258784 BP258784
c 5	43.6	18.5	901	9	AG076750 Pan trogl
6	43.4	18.4	474	2	AW984091 RC0-HN000
c 7	43.4	18.4	978	5	BU957047 AGENCOURT
c 8	40.6	17.2	910	9	CNS0060N AL065629 Drosophil
9	39.4	16.7	894	6	CD389141 AGENCOURT

c	10	39.4	16.7	957	9	CL476240	CL476240	SAIL_251_
c	11	39.2	16.6	228	9	CNS02IKT	AL199046	Tetraodon
c	12	39.2	16.6	692	9	CNS007WH	AL050923	Drosophil
	13	39.2	16.6	731	5	BX461865	BX461865	BX461865
c	14	38.8	16.4	732	2	BE790511	BE790511	601582516
	15	38.8	16.4	1047	5	BQ717248	BQ717248	AGENCOURT
	16	38.8	16.4	1399	3	CR694407	CR694407	Tetraodon
	17	38.6	16.4	682	5	BQ019180	BQ019180	UI-H-DT1-
	18	38.2	16.2	1130	2	BE909344	BE909344	601499729
c	19	38	16.1	787	9	AG167864	AG167864	Pan trogl
	20	38	16.1	966	9	CNS02RAG	AL210337	Tetraodon
	21	37.8	16.0	671	8	BH997981	BH997981	oeg69a02.
c	22	37.8	16.0	1004	9	AG276357	AG276357	Mus muscu
c	23	37.8	16.0	1201	9	CNS016C1	AL106555	Drosophil
c	24	37.8	16.0	1272	9	AG073527	AG073527	Pan trogl
	25	37.6	15.9	910	9	CNS006ON	AL065629	Drosophil
	26	37.4	15.8	798	4	BM042460	BM042460	603616292
	27	37.4	15.8	892	5	BQ428479	BQ428479	AGENCOURT
	28	37.4	15.8	941	9	AG070543	AG070543	Pan trogl
c	29	37.2	15.8	675	4	BG765097	BG765097	602737519
c	30	37.2	15.8	700	4	BI761797	BI761797	603046791
c	31	37.2	15.8	818	4	BI459466	BI459466	603200458
c	32	37.2	15.8	907	6	CB898968	CB898968	tric016xl
c	33	37.2	15.8	907	7	CF868868	CF868868	tric016xl
c	34	37.2	15.8	944	2	BF308727	BF308727	601890022
c	35	37	15.7	376	1	AI465782	AI465782	vw97e10.y
	36	37	15.7	461	8	AQ849353	AQ849353	LMAJFV1_1
	37	37	15.7	643	4	BI559431	BI559431	603252926
c	38	37	15.7	673	6	BY749647	BY749647	BY749647
c	39	37	15.7	711	5	BQ028478	BQ028478	UI-H-CO0-
	40	37	15.7	935	9	CNS006XK	AL066051	Drosophil
c	41	37	15.7	1557	9	CL508746	CL508746	SAIL_802_
c	42	37	15.7	1630	2	BE421606	BE421606	HWM011cG.
c	43	36.8	15.6	1063	4	BG809643	BG809643	mgct001xd
c	44	36.8	15.6	1121	9	AG072392	AG072392	Pan trogl
	45	36.6	15.5	297	5	BY219454	BY219454	BY219454

OM nucleic - nucleic search, using sw model

Run on: October 11, 2005, 06:09:23 ; Search time 1785.58 Seconds
 (without alignments)
 5030.955 Million cell updates/sec

Title: US-10-798-678-1
 Perfect score: 236
 Sequence: 1 cagcccatacaaggccatgg.....ttccagcacagcccagccag 236

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : EST:*
 1: gb_est1:*
 2: gb_est2:*
 3: gb_htc:*
 4: gb_est3:*
 5: gb_est4:*
 6: gb_est5:*
 7: gb_est6:*
 8: gb_gss1:*
 9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query					ID	Description
	No.	Score	Match	Length	DB		
	1	85	36.0	817	5	BP171166	BP171166 BP171166
	2	60.4	25.6	583	5	BP231401	BP231401 BP231401
	3	58	24.6	701	5	BP439864	BP439864 BP439864
	4	46	19.5	560	5	BP258784	BP258784 BP258784
c	5	43.6	18.5	901	9	AG076750	AG076750 Pan trogl
	6	43.4	18.4	474	2	AW984091	AW984091 RC0-HN000
c	7	43.4	18.4	978	5	BU957047	BU957047 AGENCOURT
c	8	40.6	17.2	910	9	CNS0060N	AL065629 Drosophil
	9	39.4	16.7	894	6	CD389141	CD389141 AGENCOURT

c	10	39.4	16.7	957	9	CL476240	CL476240	SAIL_251_
c	11	39.2	16.6	228	9	CNS02IKT	AL199046	Tetraodon
c	12	39.2	16.6	692	9	CNS007WH	AL050923	Drosophil
	13	39.2	16.6	731	5	BX461865	BX461865	BX461865
c	14	38.8	16.4	732	2	BE790511	BE790511	601582516
	15	38.8	16.4	1047	5	BQ717248	BQ717248	AGENCOURT
	16	38.8	16.4	1399	3	CR694407	CR694407	Tetraodon
	17	38.6	16.4	682	5	BQ019180	BQ019180	UI-H-DT1-
	18	38.2	16.2	1130	2	BE909344	BE909344	601499729
c	19	38	16.1	787	9	AG167864	AG167864	Pan trogl
	20	38	16.1	966	9	CNS02RAG	AL210337	Tetraodon
	21	37.8	16.0	671	8	BH997981	BH997981	oeg69a02.
c	22	37.8	16.0	1004	9	AG276357	AG276357	Mus muscu
c	23	37.8	16.0	1201	9	CNS016C1	AL106555	Drosophil
c	24	37.8	16.0	1272	9	AG073527	AG073527	Pan trogl
	25	37.6	15.9	910	9	CNS006ON	AL065629	Drosophil
	26	37.4	15.8	798	4	BM042460	BM042460	603616292
	27	37.4	15.8	892	5	BQ428479	BQ428479	AGENCOURT
	28	37.4	15.8	941	9	AG070543	AG070543	Pan trogl
c	29	37.2	15.8	675	4	BG765097	BG765097	602737519
c	30	37.2	15.8	700	4	BI761797	BI761797	603046791
c	31	37.2	15.8	818	4	BI459466	BI459466	603200458
c	32	37.2	15.8	907	6	CB898968	CB898968	tric016xl
c	33	37.2	15.8	907	7	CF868868	CF868868	tric016xl
c	34	37.2	15.8	944	2	BF308727	BF308727	601890022
c	35	37	15.7	376	1	AI465782	AI465782	vw97e10.y
	36	37	15.7	461	8	AQ849353	AQ849353	LMAJFV1_1
	37	37	15.7	643	4	BI559431	BI559431	603252926
c	38	37	15.7	673	6	BY749647	BY749647	BY749647
c	39	37	15.7	711	5	BQ028478	BQ028478	UI-H-CO0-
	40	37	15.7	935	9	CNS006XK	AL066051	Drosophil
c	41	37	15.7	1557	9	CL508746	CL508746	SAIL_802_
c	42	37	15.7	1630	2	BE421606	BE421606	HWM011cG.
c	43	36.8	15.6	1063	4	BG809643	BG809643	mgct001xd
c	44	36.8	15.6	1121	9	AG072392	AG072392	Pan trogl
	45	36.6	15.5	297	5	BY219454	BY219454	BY219454

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OM nucleic - nucleic search, using sw model

Run on: October 11, 2005, 06:09:25 ; Search time 679.618 Seconds
(without alignments)
2418.567 Million cell updates/sec

Title: US-10-798-678-1
Perfect score: 236
Sequence: 1 cagcccatacaaggccatgg.....ttccagcacagcccagccag 236

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 8443130 seqs, 3482420727 residues

Total number of hits satisfying chosen parameters: 16886260

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:*
- 22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	%		Query Match Length DB	ID	Description
	Score	Match			
1	236	100.0	236	20	US-10-798-678-1
2	122.8	52.0	655	15	US-10-156-604-18
3	89.2	37.8	591	17	US-10-149-736-61
4	89.2	37.8	591	21	US-10-964-536-61
5	87.8	37.2	4101	21	US-10-492-901-8
6	80	33.9	4476	10	US-09-845-416-31
7	76.6	32.5	365	17	US-10-149-736-93
8	76.6	32.5	365	21	US-10-964-536-93
9	76.6	32.5	951	17	US-10-149-736-92
10	76.6	32.5	951	21	US-10-964-536-92
11	76.6	32.5	955	10	US-09-845-416-26
12	76.6	32.5	4414	10	US-09-845-416-32
13	76.6	32.5	4498	10	US-09-845-416-30
14	76.6	32.5	4825	10	US-09-845-416-29
15	76.6	32.5	4966	10	US-09-845-416-28
16	76.6	32.5	5149	10	US-09-845-416-27
17	73.6	31.2	1437	9	US-09-925-302-56
18	73.6	31.2	1437	10	US-09-925-302-56
c 19	49.2	20.8	8147	15	US-10-311-455-402
20	42.6	18.1	8147	15	US-10-311-455-401
c 21	38.6	16.4	1143	17	US-10-369-493-31533
22	37.8	16.0	596	13	US-10-027-632-168629
23	37.8	16.0	596	17	US-10-027-632-168629
c 24	37.4	15.8	1404	22	US-10-450-763-29957
c 25	37	15.7	35156	19	US-10-322-281-404
c 26	36.6	15.5	526	20	US-10-425-115-177204
c 27	36.2	15.3	617	13	US-10-027-632-104647
c 28	36.2	15.3	617	17	US-10-027-632-104647
29	35.8	15.2	581	20	US-10-425-115-93481
c 30	35.8	15.2	774	13	US-10-027-632-11077
c 31	35.8	15.2	774	17	US-10-027-632-11077
c 32	35.8	15.2	1320	17	US-10-282-122A-28721
33	35.6	15.1	1800	17	US-10-094-749-1328
34	35.6	15.1	1893	20	US-10-723-860-3581
35	35.6	15.1	1893	22	US-10-756-149-3464
c 36	35.6	15.1	2133	18	US-10-363-616-145
37	35.6	15.1	2214	20	US-10-723-860-7550
38	35.2	14.9	1248	19	US-10-437-963-95459
c 39	35	14.8	445	20	US-10-372-917-4
c 40	35	14.8	448	20	US-10-372-917-1
41	35	14.8	1308	9	US-09-730-772-12
42	35	14.8	1308	9	US-09-735-849-12
43	35	14.8	1308	10	US-09-825-751A-84
44	35	14.8	1308	10	US-09-574-819-12
45	35	14.8	1308	16	US-10-379-830-12

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OM nucleic - nucleic search, using sw model

Run on: October 11, 2005, 06:09:25 ; Search time 64.7843 Seconds
(without alignments)
5960.722 Million cell updates/sec

Title: US-10-798-678-1
Perfect score: 236
Sequence: 1 cagcccatacaaggccatgg.....ttccagcacagcccagccag 236

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				Description
	No.	Score	Match	Length	ID		
	1	76.6	32.5	1361	1	US-08-530-529-1	Sequence 1, Appli
	2	76.6	32.5	1361	3	US-09-119-264-1	Sequence 1, Appli
	3	76.6	32.5	3364	2	US-08-735-609-9	Sequence 9, Appli
	4	76.6	32.5	3364	2	US-08-735-609-9	Sequence 9, Appli
	5	76.6	32.5	3364	3	US-09-315-372-9	Sequence 9, Appli
	6	76.6	32.5	3364	3	US-09-244-752-9	Sequence 9, Appli
	7	76.6	32.5	3364	3	US-09-245-497-9	Sequence 9, Appli
	8	76.6	32.5	3364	3	US-09-562-919-9	Sequence 9, Appli
c	9	39.6	16.8	1335	4	US-09-949-016-3466	Sequence 3466, Ap
c	10	39.6	16.8	44096	4	US-09-949-016-15208	Sequence 15208, A
	11	39.6	16.8	81585	4	US-09-949-016-15427	Sequence 15427, A

c	12	37	15.7	19157	4	US-09-949-016-13142	Sequence 13142, A
c	13	36.6	15.5	1806	4	US-09-252-991A-11250	Sequence 11250, A
	14	36.6	15.5	3141	4	US-09-252-991A-10937	Sequence 10937, A
	15	36	15.3	251	4	US-09-313-294A-3512	Sequence 3512, Ap
	16	36	15.3	86414	4	US-09-949-016-12345	Sequence 12345, A
	17	36	15.3	86414	4	US-09-949-016-15758	Sequence 15758, A
	18	35.8	15.2	4403765	3	US-09-103-840A-2	Sequence 2, Appli
	19	35.8	15.2	4411529	3	US-09-103-840A-1	Sequence 1, Appli
	20	34.8	14.7	134008	4	US-09-949-016-13841	Sequence 13841, A
	21	34.6	14.7	112114	4	US-09-949-016-17292	Sequence 17292, A
	22	34.6	14.7	154605	4	US-09-949-016-11894	Sequence 11894, A
c	23	34.4	14.6	1247	2	US-08-773-870-2	Sequence 2, Appli
c	24	34	14.4	109159	4	US-09-949-016-14169	Sequence 14169, A
c	25	34	14.4	109159	4	US-09-949-016-14170	Sequence 14170, A
c	26	33.6	14.2	1331	4	US-09-023-655-579	Sequence 579, App
	27	33.6	14.2	4048	4	US-09-976-594-1053	Sequence 1053, Ap
c	28	33.4	14.2	1035	4	US-09-902-540-9664	Sequence 9664, Ap
c	29	33.4	14.2	3620	4	US-09-016-434-1055	Sequence 1055, Ap
c	30	33.4	14.2	3620	4	US-09-023-655-862	Sequence 862, App
c	31	33.4	14.2	14330	4	US-09-902-540-1009	Sequence 1009, Ap
	32	33.4	14.2	44120	4	US-09-949-016-14151	Sequence 14151, A
	33	33.4	14.2	44120	4	US-09-949-016-14152	Sequence 14152, A
	34	33.4	14.2	44120	4	US-09-949-016-14153	Sequence 14153, A
	35	33.4	14.2	44120	4	US-09-949-016-14154	Sequence 14154, A
	36	33.4	14.2	44120	4	US-09-949-016-14155	Sequence 14155, A
	37	33.4	14.2	44120	4	US-09-949-016-14156	Sequence 14156, A
	38	33.2	14.1	2916	4	US-09-248-796A-5428	Sequence 5428, Ap
c	39	33	14.0	8831	4	US-09-949-016-17608	Sequence 17608, A
	40	32.8	13.9	1492	3	US-09-657-042A-10	Sequence 10, Appl
	41	32.8	13.9	3370	1	US-08-060-822A-5	Sequence 5, Appli
	42	32.8	13.9	3370	5	PCT-US94-05257-5	Sequence 5, Appli
c	43	32.8	13.9	3508	4	US-09-312-762A-1	Sequence 1, Appli
c	44	32.8	13.9	28493	4	US-09-902-540-1241	Sequence 1241, Ap
c	45	32.6	13.8	19091	4	US-09-949-016-15805	Sequence 15805, A

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OM nucleic - nucleic search, using sw model

Run on: October 11, 2005, 06:09:23 ; Search time 209.624 Seconds
(without alignments)
6664.609 Million cell updates/sec

Title: US-10-798-678-1
Perfect score: 236
Sequence: 1 cagcccatacaaggccatgg.....ttccagcacagcccagccag 236

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	235.6	99.8	236	13	ADS13172	Ads13172 Porcine c
2	127.6	54.1	2903	6	AAL44608	Aal44608 Human mus
3	122.8	52.0	655	8	ABZ20800	Abz20800 Murine MC
4	101.6	43.1	377	6	AAL44614	Aal44614 Human mus

	5	91.4	38.7	1682	6	AAL44616	Aal44616 Rat muscl
	6	89.2	37.8	594	6	ABK82019	Abk82019 Creatine
	7	87.8	37.2	4101	8	ACC47993	Acc47993 Mouse mus
	8	80	33.9	4476	6	AAD37259	Aad37259 Adeno-ass
	9	79.6	33.7	366	6	AAL44622	Aal44622 Rat muscl
	10	76.6	32.5	365	6	ABK82051	Abk82051 Mouse mus
	11	76.6	32.5	365	6	AAL44606	Aal44606 Murine mu
	12	76.6	32.5	576	6	AAL44602	Aal44602 Murine MC
	13	76.6	32.5	951	6	ABK82050	Abk82050 Mouse mus
	14	76.6	32.5	951	6	AAL44605	Aal44605 Murine mu
	15	76.6	32.5	955	6	AAD37254	Aad37254 Adeno-ass
	16	76.6	32.5	1121	6	AAL44603	Aal44603 Murine MC
	17	76.6	32.5	1263	6	AAL44604	Aal44604 Murine MC
	18	76.6	32.5	1361	2	AAT61698	Aat61698 Mouse mus
	19	76.6	32.5	3357	6	AAL44595	Aal44595 Murine mu
	20	76.6	32.5	3364	2	AAV07266	Aav07266 Muscle cr
	21	76.6	32.5	4414	6	AAD37260	Aad37260 Adeno-ass
	22	76.6	32.5	4498	6	AAD37258	Aad37258 Adeno-ass
	23	76.6	32.5	4825	6	AAD37257	Aad37257 Adeno-ass
	24	76.6	32.5	4966	6	AAD37256	Aad37256 Adeno-ass
	25	76.6	32.5	5149	6	AAD37255	Aad37255 Adeno-ass
	26	73.6	31.2	1437	3	AAF18037	Aaf18037 Lung canc
c	27	49.2	20.8	8147	6	ABL32429	Abl32429 Human imm
	28	44	18.6	87	6	AAL44615	Aal44615 Human mus
	29	42.6	18.1	8147	6	ABL32428	Abl32428 Human imm
c	30	38.6	16.4	1143	13	ADS55859	Ads55859 Bacterial
	31	37.8	16.0	2277	4	AAK82195	Aak82195 Human imm
c	32	37.4	15.8	1404	5	AAS94153	Aas94153 DNA encod
c	33	37	15.7	35156	13	ABD33329	Abd33329 Human can
c	34	36.6	15.5	1806	11	ABD12646	Abd12646 Pseudomon
	35	36.6	15.5	3141	11	ABD12333	Abd12333 Pseudomon
	36	36.2	15.3	5349	3	AAA65527	Aaa65527 Porcine B
	37	36	15.3	251	10	ABX85052	Abx85052 Corn ear-
c	38	35.8	15.2	1320	8	ACA40851	Aca40851 Prokaryot
	39	35.8	15.2	110000	4	AAI99682_40	Continuation (41 o
	40	35.8	15.2	110000	4	AAI99683_40	Continuation (41 o
	41	35.6	15.1	1800	10	ADA53760	Ada53760 Human cod
	42	35.6	15.1	1893	12	ADQ20761	Adq20761 Human sof
c	43	35.6	15.1	2133	6	ABQ93432	Abq93432 Human cDN
	44	35.6	15.1	2214	12	ADQ24730	Adq24730 Human sof
c	45	35	14.8	553	6	ABT10269	Abt10269 Human bre

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OM nucleic - nucleic search, using sw model

Run on: October 11, 2005, 06:09:23 ; Search time 279.942 Seconds
(without alignments)
5030.955 Million cell updates/sec

Title: US-10-798-678-8
Perfect score: 37
Sequence: 1 ctggctgggctgtgctggaatatcctggaggcgacac 37

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	23.6	63.8	748	7	CV114754	CV114754 AGENCOURT
	2	23.2	62.7	517	8	BZ940512	BZ940512 CH240_107
c	3	23.2	62.7	853	9	CR828489	CR828489 GR0AAA6DD
	4	22.8	61.6	790	5	BQ752402	BQ752402 EST632965
c	5	22.8	61.6	801	5	BQ752403	BQ752403 EST632966
c	6	22.6	61.1	456	6	CB740424	CB740424 AMGNNUC:N
	7	22.4	60.5	763	5	BU937041	BU937041 AGENCOURT
c	8	22.4	60.5	796	5	BU600431	BU600431 AGENCOURT

c	9	22.2	60.0	746	7	CO556166	CO556166	AGENCOURT
c	10	22.2	60.0	790	5	BQ752344	BQ752344	EST632907
c	11	22	59.5	461	8	AQ662841	AQ662841	HS_5480_A
c	12	22	59.5	685	2	BB104830	BB104830	BB104830
c	13	22	59.5	788	9	CR045505	CR045505	Forward s
c	14	22	59.5	3373	3	AK035140	AK035140	Mus muscu
c	15	21.8	58.9	252	2	BF388177	BF388177	UI-R-CA1-
	16	21.8	58.9	624	8	AZ292868	AZ292868	RPCI-23-1
	17	21.8	58.9	676	4	BM448567	BM448567	DSA025E09
	18	21.8	58.9	777	7	CO003345	CO003345	EST791680
	19	21.8	58.9	818	5	BU200732	BU200732	603951273
c	20	21.8	58.9	888	7	CO012012	CO012012	EST800347
	21	21.8	58.9	912	7	CO012013	CO012013	EST800348
	22	21.8	58.9	1041	9	CNS0011P	AL074319	Drosophil
c	23	21.6	58.4	188	1	AV607783	AV607783	AV607783
c	24	21.6	58.4	253	8	AZ909607	AZ909607	RPCI-24-1
c	25	21.6	58.4	354	5	BP755692	BP755692	BP755692
	26	21.6	58.4	384	2	AW312854	AW312854	5200 MARC
	27	21.6	58.4	399	6	CD804324	CD804324	UI-M-GV0-
c	28	21.6	58.4	402	2	AW551033	AW551033	L0072F09-
	29	21.6	58.4	403	2	BB671984	BB671984	BB671984
c	30	21.6	58.4	407	2	AW049492	AW049492	UI-M-BH1-
c	31	21.6	58.4	411	5	BP755845	BP755845	BP755845
c	32	21.6	58.4	412	4	BI244198	BI244198	Eg_PSGR_0
	33	21.6	58.4	414	1	AA914113	AA914113	vy92c09.r
	34	21.6	58.4	416	2	BB688529	BB688529	BB688529
	35	21.6	58.4	420	8	BZ834344	BZ834344	CH240_222
c	36	21.6	58.4	423	2	BE945424	BE945424	UI-M-BZ0-
	37	21.6	58.4	428	6	BY639824	BY639824	BY639824
c	38	21.6	58.4	441	5	BP753783	BP753783	BP753783
c	39	21.6	58.4	450	5	BP754635	BP754635	BP754635
	40	21.6	58.4	451	1	AA265823	AA265823	mz71e06.r
c	41	21.6	58.4	451	4	BM120887	BM120887	L0945D03-
c	42	21.6	58.4	464	5	BP767900	BP767900	BP767900
c	43	21.6	58.4	465	4	BM118156	BM118156	L0861G09-
	44	21.6	58.4	493	1	AL805051	AL805051	AL805051
	45	21.6	58.4	499	6	CD803976	CD803976	UI-M-GV0-

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OM nucleic - nucleic search, using sw model

Run on: October 11, 2005, 06:09:25 ; Search time 106.55 Seconds
(without alignments)
2418.567 Million cell updates/sec

Title: US-10-798-678-8
Perfect score: 37
Sequence: 1 ctggctgggctgtgctggaatatcctggaggcgacac 37

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 8443130 seqs, 3482420727 residues

Total number of hits satisfying chosen parameters: 16886260

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:*
- 22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	37	100.0	37	20	US-10-798-678-8	Sequence 8, Appli
	2	22.6	61.1	68732	19	US-10-322-281-560	Sequence 560, App
c	3	22.2	60.0	600	22	US-10-972-079-22942	Sequence 22942, A
	4	21.8	58.9	307	18	US-10-424-599-59566	Sequence 59566, A
	5	21.6	58.4	460	19	US-10-430-201-2005	Sequence 2005, Ap
	6	21.6	58.4	460	19	US-10-430-201-2006	Sequence 2006, Ap
	7	21.6	58.4	812	13	US-10-027-632-143753	Sequence 143753,
	8	21.6	58.4	812	17	US-10-027-632-143753	Sequence 143753,
c	9	21.4	57.8	201	21	US-10-741-600-32098	Sequence 32098, A
c	10	21.4	57.8	201	21	US-10-741-600-32100	Sequence 32100, A
c	11	21.4	57.8	201	21	US-10-741-600-32102	Sequence 32102, A
c	12	21.4	57.8	201	21	US-10-741-600-32103	Sequence 32103, A
c	13	21.4	57.8	201	21	US-10-741-600-32491	Sequence 32491, A
c	14	21.4	57.8	593	22	US-10-450-763-5551	Sequence 5551, Ap
c	15	21.4	57.8	593	22	US-10-450-763-6753	Sequence 6753, Ap
c	16	21.4	57.8	1131	22	US-10-450-763-5542	Sequence 5542, Ap
c	17	21.4	57.8	1131	22	US-10-450-763-6748	Sequence 6748, Ap
	18	21.4	57.8	81748	13	US-10-087-192-364	Sequence 364, App
c	19	21.4	57.8	118356	21	US-10-741-600-17643	Sequence 17643, A
	20	21.4	57.8	394468	21	US-10-741-600-17952	Sequence 17952, A
c	21	21.2	57.3	453	9	US-09-893-737-1	Sequence 1, Appli
c	22	21.2	57.3	453	22	US-10-970-713-1	Sequence 1, Appli
c	23	21.2	57.3	654	17	US-10-282-122A-28807	Sequence 28807, A
c	24	21.2	57.3	698	13	US-10-027-632-163642	Sequence 163642,
c	25	21.2	57.3	698	17	US-10-027-632-163642	Sequence 163642,
	26	21	56.8	828	14	US-10-198-846-67	Sequence 67, Appl
	27	21	56.8	919	14	US-10-198-846-10250	Sequence 10250, A
	28	21	56.8	1194	19	US-10-375-266-33	Sequence 33, Appl
	29	21	56.8	1278	15	US-10-156-761-5081	Sequence 5081, Ap
c	30	21	56.8	9025608	15	US-10-156-761-1	Sequence 1, Appli
	31	20.8	56.2	291	9	US-09-969-708-444	Sequence 444, App
	32	20.8	56.2	291	21	US-10-843-641A-7915	Sequence 7915, Ap
c	33	20.8	56.2	351	9	US-09-777-564-1223	Sequence 1223, Ap
c	34	20.8	56.2	351	14	US-10-015-219-1223	Sequence 1223, Ap
c	35	20.8	56.2	902	22	US-10-783-271-105	Sequence 105, App
c	36	20.8	56.2	928	16	US-10-231-417-84	Sequence 84, Appl
c	37	20.8	56.2	3479	9	US-09-822-849A-298	Sequence 298, App
	38	20.8	56.2	133100	22	US-10-723-681-4	Sequence 4, Appli
c	39	20.8	56.2	238417	21	US-10-461-862-98	Sequence 98, Appl
c	40	20.6	55.7	150	17	US-10-242-535A-828	Sequence 828, App
c	41	20.6	55.7	150	18	US-10-085-783A-828	Sequence 828, App
c	42	20.6	55.7	333	9	US-09-560-863-310	Sequence 310, App
	43	20.6	55.7	468	9	US-09-864-761-6002	Sequence 6002, Ap
	44	20.6	55.7	549	13	US-10-027-632-275490	Sequence 275490,
	45	20.6	55.7	549	17	US-10-027-632-275490	Sequence 275490,

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OM nucleic - nucleic search, using sw model

Run on: October 11, 2005, 06:09:25 ; Search time 10.1569 Seconds
(without alignments)
5960.722 Million cell updates/sec

Title: US-10-798-678-8
Perfect score: 37
Sequence: 1 ctggctgggctgtgctggaatatcctggaggcgacac 37

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				ID	Description
	No.	Score	Match	Length	DB	Query		
c	1	22.6	61.1	601	4	US-09-949-016-131207		Sequence 131207,
	2	22.6	61.1	199945	4	US-09-949-016-15436		Sequence 15436, A
c	3	21.2	57.3	453	4	US-09-893-737-1		Sequence 1, Appli
	4	21	56.8	13102	4	US-09-949-016-17552		Sequence 17552, A
	5	20.8	56.2	39489	4	US-09-949-016-13886		Sequence 13886, A
	6	20.8	56.2	70828	4	US-09-949-016-12122		Sequence 12122, A
c	7	20.8	56.2	139150	4	US-09-949-016-17398		Sequence 17398, A
c	8	20.8	56.2	139577	4	US-09-949-016-12879		Sequence 12879, A
	9	20.6	55.7	28203	4	US-09-949-016-16952		Sequence 16952, A
	10	20.6	55.7	28203	4	US-09-949-016-16953		Sequence 16953, A
	11	20.6	55.7	28203	4	US-09-949-016-16954		Sequence 16954, A

	12	20.6	55.7	36090	4	US-09-949-016-17424	Sequence 17424, A
	13	20.6	55.7	36123	4	US-09-949-016-12402	Sequence 12402, A
	14	20.4	55.1	477	4	US-09-902-540-9521	Sequence 9521, Ap
c	15	20.4	55.1	601	4	US-09-949-016-175279	Sequence 175279,
	16	20.4	55.1	13805	4	US-09-902-540-1083	Sequence 1083, Ap
c	17	20.4	55.1	33152	4	US-09-949-016-16719	Sequence 16719, A
c	18	20.2	54.6	601	4	US-09-949-016-137847	Sequence 137847,
c	19	20.2	54.6	1471	3	US-09-492-985-11	Sequence 11, Appl
	20	20.2	54.6	2311	3	US-08-976-259-26	Sequence 26, Appl
	21	20.2	54.6	2311	4	US-09-956-004-26	Sequence 26, Appl
	22	20.2	54.6	61847	4	US-09-949-016-16677	Sequence 16677, A
c	23	20.2	54.6	77626	4	US-09-949-016-12608	Sequence 12608, A
c	24	20.2	54.6	135171	4	US-09-949-016-15617	Sequence 15617, A
c	25	20	54.1	601	4	US-09-949-016-175277	Sequence 175277,
c	26	20	54.1	601	4	US-09-949-016-175278	Sequence 175278,
c	27	20	54.1	805	4	US-09-270-767-10645	Sequence 10645, A
	28	20	54.1	1773	4	US-09-194-949A-14	Sequence 14, Appl
	29	20	54.1	3496	4	US-09-042-460-1	Sequence 1, Appli
	30	19.8	53.5	1196	4	US-09-270-767-11242	Sequence 11242, A
c	31	19.8	53.5	5654	4	US-09-573-080A-41	Sequence 41, Appl
	32	19.8	53.5	43537	4	US-09-949-016-13458	Sequence 13458, A
c	33	19.8	53.5	83349	4	US-09-949-016-17149	Sequence 17149, A
	34	19.8	53.5	111677	4	US-09-949-016-16946	Sequence 16946, A
c	35	19.8	53.5	148156	4	US-09-949-016-11776	Sequence 11776, A
	36	19.8	53.5	636591	4	US-09-949-016-11808	Sequence 11808, A
	37	19.8	53.5	636591	4	US-09-949-016-13388	Sequence 13388, A
c	38	19.6	53.0	207	4	US-09-328-352-3424	Sequence 3424, Ap
	39	19.6	53.0	870	4	US-09-489-039A-5219	Sequence 5219, Ap
	40	19.6	53.0	3661	4	US-09-893-371A-3	Sequence 3, Appli
c	41	19.6	53.0	15602	3	US-09-844-634-17	Sequence 17, Appl
c	42	19.6	53.0	34094	4	US-09-292-034-1	Sequence 1, Appli
c	43	19.6	53.0	46253	4	US-09-949-016-11890	Sequence 11890, A
c	44	19.6	53.0	46257	4	US-09-949-016-13711	Sequence 13711, A
	45	19.6	53.0	47727	4	US-09-949-016-12904	Sequence 12904, A

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OM nucleic - nucleic search, using sw model

Run on: October 11, 2005, 06:09:23 ; Search time 32.8647 Seconds
(without alignments)
6664.609 Million cell updates/sec

Title: US-10-798-678-8
Perfect score: 37
Sequence: 1 ctggctgggctgtgctggaatatcctggaggcgacac 37

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	37	100.0	37	13	ADS13179		Ads13179 PCR prime
2	22.6	61.1	68732	13	ABD33428		Abd33428 Human can
3	21.6	58.4	460	12	ADL85613		Adl85613 DNA up-re
4	21.6	58.4	460	12	ADL85612		Adl85612 DNA up-re

c	5	21.4	57.8	593	5	AAS69747	Aas69747 DNA encod
c	6	21.4	57.8	593	5	AAS70949	Aas70949 DNA encod
c	7	21.4	57.8	1131	5	AAS70944	Aas70944 DNA encod
c	8	21.4	57.8	1131	5	AAS69738	Aas69738 DNA encod
	9	21.4	57.8	81748	11	ACN44090	Acn44090 Human gen
c	10	21.2	57.3	453	6	ABK32990	Abk32990 DNA encod
c	11	21.2	57.3	654	8	ACA40937	Aca40937 Prokaryot
	12	21	56.8	241	4	AAL16969	Aal16969 Human bre
	13	21	56.8	256	4	AAL08690	Aal08690 Human bre
	14	21	56.8	257	3	AAA43124	Aaa43124 Human sec
	15	21	56.8	828	11	ACN78917	Acn78917 Breast ca
	16	21	56.8	919	11	ACN89100	Acn89100 Breast ca
	17	21	56.8	1194	13	ADR44413	Adr44413 M. methyl
	18	20.8	56.2	291	6	ABL69578	Abl69578 Prostate
c	19	20.8	56.2	351	4	AAS25042	Aas25042 Human ova
c	20	20.8	56.2	464	5	AAH83687	Aah83687 Human ova
c	21	20.8	56.2	902	13	ACN39276	Acn39276 Tumour-as
c	22	20.8	56.2	928	2	AAX61395	Aax61395 DNA encod
	23	20.8	56.2	2712	6	ABX17318	Abx17318 Human can
c	24	20.8	56.2	2836	12	ADQ64830	Adq64830 Novel hum
c	25	20.8	56.2	3479	6	ABK35160	Abk35160 Human cDN
	26	20.8	56.2	7989	4	AAK78288	Aak78288 Human imm
	27	20.8	56.2	133100	12	ADP45594	Adp45594 Human NUM
c	28	20.8	56.2	152141	8	ACA64961	Aca64961 Human BCR
c	29	20.8	56.2	238417	13	ABD32868	Abd32868 Human can
c	30	20.6	55.7	333	8	ABX64703	Abx64703 Human gen
	31	20.6	55.7	468	4	ABA58446	Aba58446 Human foe
	32	20.6	55.7	468	4	AAI38092	Aai38092 Probe #67
	33	20.6	55.7	468	4	ABA27536	Aba27536 Probe #60
	34	20.6	55.7	468	4	AAK32240	Aak32240 Human bon
	35	20.6	55.7	468	4	AAK06553	Aak06553 Human bra
	36	20.6	55.7	468	4	ABS31942	Abs31942 Human liv
	37	20.6	55.7	468	6	ABS07013	Abs07013 Human gen
	38	20.6	55.7	17104	4	AAS30249	Aas30249 DNA encod
	39	20.6	55.7	17104	4	AAS33484	Aas33484 DNA encod
	40	20.6	55.7	17104	4	AAS26973	Aas26973 Human gen
	41	20.6	55.7	17104	8	ACD01504	Acd01504 Human gen
	42	20.6	55.7	17107	4	AAS30248	Aas30248 DNA encod
	43	20.6	55.7	17107	4	AAS33483	Aas33483 DNA encod
	44	20.6	55.7	17107	4	AAS26972	Aas26972 Human gen
	45	20.6	55.7	17107	8	ACD01503	Acd01503 Human gen

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OM nucleic - nucleic search, using sw model

Run on: October 11, 2005, 06:09:23 ; Search time 177.721 Seconds
(without alignments)
10087.968 Million cell updates/sec

Title: US-10-798-678-8
Perfect score: 37
Sequence: 1 ctggctgggctgtgctggaatatcctggaggcgacac 37

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	25	67.6	50488	9	AL133231	AL133231 Human DNA
c 2	25	67.6	160536	2	AC040953	AC040953 Homo sapi
c 3	24.2	65.4	179877	2	AC102051	AC102051 Mus muscu

c	4	24.2	65.4	198033	10	AL732399	AL732399 Mouse DNA
	5	24.2	65.4	220893	2	AC102058	AC102058 Mus muscu
	6	24	64.9	249683	2	AC119541	AC119541 Rattus no
	7	23.8	64.3	579	9	GGIGE2C1	X08045 Gorilla imm
c	8	23.2	62.7	193017	2	AC150485	AC150485 Bos tauru
	9	23	62.2	86618	9	HS593F22	AL030999 Human DNA
	10	23	62.2	103916	9	AC004225	AC004225 Homo sapi
	11	23	62.2	110000	2	AL732359_08	Continuation (9 of
	12	23	62.2	123241	2	AC022090	AC022090 Homo sapi
c	13	23	62.2	125837	9	AC016553	AC016553 Homo sapi
c	14	23	62.2	134580	2	AC025359	AC025359 Homo sapi
	15	23	62.2	200087	9	AL354821	AL354821 Human DNA
c	16	22.8	61.6	57634	2	AC149539	AC149539 Xenopus t
	17	22.8	61.6	76388	2	AC151335	AC151335 Xenopus t
	18	22.8	61.6	179883	2	AC007721	AC007721 Homo sapi
	19	22.8	61.6	188896	9	AL136221	AL136221 Human DNA
	20	22.8	61.6	224645	2	AC094037	AC094037 Rattus no
c	21	22.8	61.6	269916	2	AC132650	AC132650 Rattus no
c	22	22.6	61.1	103216	9	HSDJ93P18	AL080251 Human DNA
c	23	22.6	61.1	113733	9	AP003159	AP003159 Homo sapi
c	24	22.6	61.1	158666	2	AC112981	AC112981 Mus muscu
c	25	22.6	61.1	159096	9	AL161781	AL161781 Human DNA
	26	22.6	61.1	185147	2	AP002388	AP002388 Homo sapi
	27	22.6	61.1	219774	2	AC095136	AC095136 Rattus no
c	28	22.4	60.5	72249	2	AC150256	AC150256 Aedes aeg
	29	22.4	60.5	204710	2	AC148852	AC148852 Otolemur
c	30	22.4	60.5	204710	2	AC148852	AC148852 Otolemur
	31	22.4	60.5	213478	2	AC149854	AC149854 Papio anu
c	32	22.4	60.5	221604	2	AC109935	AC109935 Rattus no
	33	22.4	60.5	240525	2	AC096895	AC096895 Rattus no
	34	22.2	60.0	178965	10	AL844144	AL844144 Mouse DNA
c	35	22.2	60.0	186596	2	AC141432	AC141432 Homo sapi
	36	22.2	60.0	241189	2	AC107644	AC107644 Mus muscu
	37	22	59.5	4089	3	TFU66074	U66074 Tritrichomo
	38	22	59.5	100587	2	AC138147	AC138147 Polypteru
c	39	22	59.5	121242	9	AC126564	AC126564 Homo sapi
	40	22	59.5	169201	10	AC134337	AC134337 Mus muscu
c	41	22	59.5	176733	9	AC092850	AC092850 Homo sapi
c	42	22	59.5	188993	10	AC122000	AC122000 Mus muscu
c	43	21.8	58.9	100786	2	AC013972	AC013972 Drosophil
	44	21.8	58.9	110338	3	AC006066	AC006066 Drosophil
c	45	21.8	58.9	153749	3	AC093098	AC093098 Drosophil

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OM nucleic - nucleic search, using sw model

Run on: October 11, 2005, 06:09:23 ; Search time 151.32 Seconds
(without alignments)
5030.955 Million cell updates/sec

Title: US-10-798-678-7
Perfect score: 20
Sequence: 1 cagcccatacaaggccatgg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	ID	Description	
1	18.4	92.0	332	6	BY780881	BY780881 BY780881	
2	18.4	92.0	362	5	BY162009	BY162009 BY162009	
3	18.4	92.0	371	5	BY294899	BY294899 BY294899	
4	18.4	92.0	441	4	BG554838	BG554838 dac31h04.	
5	18.4	92.0	514	4	BJ066537	BJ066537 BJ066537	
6	18.4	92.0	531	4	BJ035843	BJ035843 BJ035843	
7	18.4	92.0	573	4	BJ040425	BJ040425 BJ040425	
8	18.4	92.0	598	5	BQ387874	BQ387874 NISC_mn26	

9	18.4	92.0	710	5	BP683305	BP683305	BP683305
10	18.4	92.0	718	3	AF549992	AF549992	Xenopus 1
11	18.4	92.0	818	6	CA791778	CA791778	AGENCOURT
12	18.4	92.0	830	5	BP672868	BP672868	BP672868
13	18.4	92.0	832	6	CA788568	CA788568	AGENCOURT
14	18.4	92.0	833	5	BP680158	BP680158	BP680158
15	18.4	92.0	833	6	CA792169	CA792169	AGENCOURT
16	18.4	92.0	848	5	BP686484	BP686484	BP686484
17	18.4	92.0	858	6	CA986763	CA986763	AGENCOURT
18	18.4	92.0	881	5	BQ736145	BQ736145	AGENCOURT
19	18.4	92.0	884	5	BQ735152	BQ735152	AGENCOURT
20	18.4	92.0	888	5	BQ735457	BQ735457	AGENCOURT
21	18.4	92.0	894	6	CA791735	CA791735	AGENCOURT
22	18.4	92.0	898	5	BQ737596	BQ737596	AGENCOURT
c 23	18.4	92.0	978	5	BQ894053	BQ894053	AGENCOURT
24	18.4	92.0	2692	3	BC043904	BC043904	Xenopus 1
25	18	90.0	714	2	BF628472	BF628472	HVSMEb000
26	17.4	87.0	350	6	BY776102	BY776102	BY776102
27	17.4	87.0	455	5	BY272335	BY272335	BY272335
c 28	17.4	87.0	568	7	CF615371	CF615371	CES013400
c 29	17.4	87.0	575	6	CA837950	CA837950	MCT011B09
c 30	17.4	87.0	589	6	CA838241	CA838241	MCT014D08
31	17.4	87.0	625	7	CK888734	CK888734	SGP160730
32	17.4	87.0	657	6	C89102	C89102	C89102 Mous
c 33	17.4	87.0	685	6	CA838842	CA838842	MCT021A06
c 34	17.4	87.0	721	4	BM658144	BM658144	MCR060E09
c 35	17	85.0	386	2	AW761895	AW761895	ur51c02.y
36	17	85.0	542	5	BQ348272	BQ348272	MR0-HT016
c 37	17	85.0	547	7	CR629352	CR629352	DKFZp468B
c 38	17	85.0	800	7	CR765245	CR765245	DKFZp468N
c 39	17	85.0	941	5	BQ949485	BQ949485	AGENCOURT
40	17	85.0	1090	6	CA276193	CA276193	SCCCSD109
41	16.8	84.0	142	6	CD551716	CD551716	B0332D10-
42	16.8	84.0	164	7	CR382824	CR382824	CR382824
43	16.8	84.0	168	2	BB588778	BB588778	BB588778
44	16.8	84.0	200	2	BB580860	BB580860	BB580860
45	16.8	84.0	200	4	BM875949	BM875949	if85e01.y

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OM nucleic - nucleic search, using sw model

Run on: October 11, 2005, 06:09:23 ; Search time 96.0654 Seconds
(without alignments)
10087.968 Million cell updates/sec

Title: US-10-798-678-7
Perfect score: 20
Sequence: 1 cagcccatacaaggccatgg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	20	100.0	365	6	AX395375	AX395375	Sequence
2	20	100.0	365	6	AX538673	AX538673	Sequence
3	20	100.0	366	6	AX395391	AX395391	Sequence

	4	20	100.0	377	6	AX395383	AX395383 Sequence
	5	20	100.0	576	6	AX395371	AX395371 Sequence
	6	20	100.0	591	6	AX538641	AX538641 Sequence
	7	20	100.0	951	6	AX395374	AX395374 Sequence
	8	20	100.0	951	6	AX538672	AX538672 Sequence
	9	20	100.0	1059	10	MUSCKM1	M13642 Mouse muscl
	10	20	100.0	1121	6	AX395372	AX395372 Sequence
	11	20	100.0	1263	6	AX395373	AX395373 Sequence
	12	20	100.0	1361	6	AR024207	AR024207 Sequence
	13	20	100.0	1361	6	AR176159	AR176159 Sequence
	14	20	100.0	1682	6	AX395385	AX395385 Sequence
	15	20	100.0	1682	10	RATCKMUSCL	M27092 Rattus norv
	16	20	100.0	2903	6	AX395377	AX395377 Sequence
	17	20	100.0	2903	9	HUMCKMM1	M21487 Human muscl
	18	20	100.0	3357	6	AX395364	AX395364 Sequence
	19	20	100.0	3357	10	AF188002	AF188002 Mus muscu
	20	20	100.0	3364	6	AR091541	AR091541 Sequence
	21	20	100.0	3364	6	AR102234	AR102234 Sequence
	22	20	100.0	3364	6	AR230732	AR230732 Sequence
	23	20	100.0	4101	10	MUSMCKA	M21390 Mouse muscl
	24	20	100.0	20454	9	AY585238	AY585238 Homo sapi
c	25	20	100.0	44052	9	AC005781	AC005781 Homo sapi
c	26	20	100.0	155060	2	AC140158	AC140158 Felis cat
c	27	20	100.0	156383	2	AC135221	AC135221 Felis cat
	28	20	100.0	160069	2	AC023329	AC023329 Homo sapi
c	29	20	100.0	163038	2	AC135542	AC135542 Pan trogl
	30	20	100.0	166513	2	AC073787	AC073787 Mus muscu
c	31	20	100.0	188698	2	AC137531	AC137531 Papio anu
c	32	20	100.0	196427	10	AC118017	AC118017 Mus muscu
c	33	20	100.0	201842	2	AC137646	AC137646 Rattus no
c	34	20	100.0	252619	2	AC095012	AC095012 Rattus no
c	35	20	100.0	260849	2	AC119447	AC119447 Rattus no
c	36	20	100.0	316822	2	AC118016	AC118016 Mus muscu
c	37	18.4	92.0	203700	2	AC141140	AC141140 Rattus no
c	38	18.4	92.0	226904	2	AC111606	AC111606 Rattus no
	39	18.4	92.0	263029	2	AC099263	AC099263 Rattus no
c	40	17.4	87.0	287	8	BPR489192	AJ489192 Beta proc
c	41	17.4	87.0	62464	9	AL159164	AL159164 Human DNA
	42	17.4	87.0	78229	9	AL139140	AL139140 Human DNA
	43	17.4	87.0	96596	6	AX695395	AX695395 Sequence
c	44	17.4	87.0	110000	1	AE017282_02	Continuation (3 of
	45	17.4	87.0	148846	10	AL591204	AL591204 Mouse DNA

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OM nucleic - nucleic search, using sw model

Run on: October 11, 2005, 06:09:23 ; Search time 151.32 Seconds
(without alignments)
5030.955 Million cell updates/sec

Title: US-10-798-678-10
Perfect score: 20
Sequence: 1 cagcccacgggtcatgatgaa 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query		DB	ID	Description
			Match	Length			
c	1	20	100.0	192	7	R86587	R86587 RABEST162T
c	2	20	100.0	195	7	R86565	R86565 RABEST139T
c	3	20	100.0	205	7	CR791328	CR791328 DKFZp468H
c	4	20	100.0	247	7	R86514	R86514 RABEST208T
c	5	20	100.0	250	6	C05347	C05347 C05347 Huma
c	6	20	100.0	260	1	AL601227	AL601227 DKFZp313G
c	7	20	100.0	271	1	AA346248	AA346248 EST52360
	8	20	100.0	280	6	CD169664	CD169664 MM1-0024T

	9	20	100.0	280	6	CD169724	CD169724 MM1-0024T
c	10	20	100.0	285	6	C05338	C05338 C05338 Huma
c	11	20	100.0	285	7	F00890	F00890 HSB78D062 S
c	12	20	100.0	286	1	AA196868	AA196868 zq09a05.r
c	13	20	100.0	291	1	AA321919	AA321919 EST24505
c	14	20	100.0	294	1	AA193072	AA193072 zp94b11.r
c	15	20	100.0	296	2	BF126218	BF126218 601650291
c	16	20	100.0	319	6	C05317	C05317 C05317 Huma
c	17	20	100.0	322	7	CR558723	CR558723 DKFZp468P
c	18	20	100.0	322	7	R57025	R57025 F0275 Fetal
c	19	20	100.0	337	7	F01081	F01081 HSBA0A042 S
c	20	20	100.0	339	7	F01275	F01275 HSBC3D052 S
c	21	20	100.0	343	7	CR752747	CR752747 DKFZp468M
c	22	20	100.0	344	7	F01305	F01305 HSBC6G022 S
c	23	20	100.0	346	7	CR549486	CR549486 DKFZp468I
c	24	20	100.0	350	2	BF576576	BF576576 602134920
c	25	20	100.0	353	6	C04866	C04866 C04866 Huma
c	26	20	100.0	357	7	CR549607	CR549607 DKFZp468O
c	27	20	100.0	362	1	AA346252	AA346252 EST52364
c	28	20	100.0	367	1	AA346031	AA346031 EST52146
c	29	20	100.0	379	7	CR753127	CR753127 DKFZp468N
c	30	20	100.0	382	2	AW481525	AW481525 36441 MAR
	31	20	100.0	387	6	CD612911	CD612911 56040720H
c	32	20	100.0	388	6	CD612912	CD612912 56040720J
	33	20	100.0	393	6	CD612913	CD612913 56040828H
	34	20	100.0	393	6	CD612915	CD612915 56040836H
c	35	20	100.0	394	6	CD612914	CD612914 56040828J
c	36	20	100.0	394	6	CD612916	CD612916 56040836J
c	37	20	100.0	398	1	AA192585	AA192585 zq01e04.r
c	38	20	100.0	398	7	CR549573	CR549573 DKFZp468N
	39	20	100.0	403	6	CD612907	CD612907 56037355H
c	40	20	100.0	409	1	AA100565	AA100565 zn51e05.r
c	41	20	100.0	411	1	AA112038	AA112038 zn53a10.r
c	42	20	100.0	411	1	AA178866	AA178866 zp38a10.r
c	43	20	100.0	411	6	C03536	C03536 C03536 Huma
c	44	20	100.0	411	7	CR789252	CR789252 DKFZp468A
c	45	20	100.0	412	6	C05600	C05600 C05600 Huma

GenCore version 5.1.6

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OM.nucleic - nucleic search, using sw model

```
Run on:      October 11, 2005, 06:09:25 ; Search time 57.5948 Seconds  
            (without alignments)  
            2418.567 Million cell updates/sec
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Title: US-10-798-678-10
Perfect score: 20
Sequence: 1 cagcccacgggtcatgatgaa 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 8443130 seqs, 3482420727 residues

Total number of hits satisfying chosen parameters: 16886260

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq:*
21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:*
22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
```


Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				
No.	Score	Query	Match	Length	DB	ID	Description
1	20	100.0	20	20	20	US-10-798-678-10	Sequence 10, Appl
c 2	20	100.0	398	10	10	US-09-918-995-5030	Sequence 5030, Ap
c 3	20	100.0	419	10	10	US-09-918-995-5159	Sequence 5159, Ap
c 4	20	100.0	1143	16	16	US-10-412-222-2	Sequence 2, Appli
c 5	20	100.0	1143	16	16	US-10-412-233-2	Sequence 2, Appli
c 6	20	100.0	1437	9	9	US-09-925-302-56	Sequence 56, Appl
c 7	20	100.0	1437	10	10	US-09-925-302-56	Sequence 56, Appl
c 8	20	100.0	1562	18	18	US-10-276-775-14	Sequence 14, Appl
c 9	20	100.0	1563	9	9	US-09-765-231A-29	Sequence 29, Appl
c 10	20	100.0	1620	21	21	US-10-367-057-163	Sequence 163, App
c 11	20	100.0	3016	18	18	US-10-641-643-259	Sequence 259, App
c 12	18.4	92.0	452	10	10	US-09-918-995-26422	Sequence 26422, A
c 13	18.4	92.0	1143	16	16	US-10-412-222-4	Sequence 4, Appli
c 14	18.4	92.0	1143	16	16	US-10-412-233-4	Sequence 4, Appli
c 15	18.4	92.0	1360	9	9	US-09-880-107-2269	Sequence 2269, Ap
c 16	18.4	92.0	1360	10	10	US-09-873-367C-707	Sequence 707, App
c 17	18.4	92.0	1360	21	21	US-10-843-641A-707	Sequence 707, App
18	18.4	92.0	1390	17	17	US-10-264-049-261	Sequence 261, App
c 19	18.4	92.0	1431	21	21	US-10-887-553A-184	Sequence 184, App
c 20	18.4	92.0	1431	22	22	US-10-764-425-7	Sequence 7, Appli
c 21	18.4	92.0	1431	24	24	US-11-019-829-5	Sequence 5, Appli
c 22	18.4	92.0	1432	17	17	US-10-133-937-3	Sequence 3, Appli
c 23	18.4	92.0	1432	17	17	US-10-159-563-3	Sequence 3, Appli
c 24	18.4	92.0	1432	17	17	US-10-159-563-191	Sequence 191, App
c 25	18.4	92.0	1432	19	19	US-10-755-889-271	Sequence 271, App
c 26	18.4	92.0	1589	19	19	US-10-605-708A-3	Sequence 3, Appli
c 27	18.4	92.0	4175	22	22	US-10-737-082-122	Sequence 122, App
c 28	18.4	92.0	4175	22	22	US-10-765-790-122	Sequence 122, App
c 29	17	85.0	378	9	9	US-09-960-352-1959	Sequence 1959, Ap
c 30	17	85.0	381	9	9	US-09-960-352-6969	Sequence 6969, Ap
c 31	17	85.0	408	9	9	US-09-960-352-9549	Sequence 9549, Ap
c 32	17	85.0	996	11	11	US-09-876-143-1347	Sequence 1347, Ap
c 33	16.8	84.0	258	14	14	US-10-284-985-22	Sequence 22, Appl
34	16.8	84.0	600	22	22	US-10-972-079-54955	Sequence 54955, A
35	16.8	84.0	600	22	22	US-10-972-079-54956	Sequence 54956, A
36	16.8	84.0	823	13	13	US-10-027-632-172970	Sequence 172970,
37	16.8	84.0	823	13	13	US-10-027-632-172971	Sequence 172971,
38	16.8	84.0	823	17	17	US-10-027-632-172970	Sequence 172970,
39	16.8	84.0	823	17	17	US-10-027-632-172971	Sequence 172971,
c 40	16.8	84.0	1035	10	10	US-09-899-575-10	Sequence 10, Appl
c 41	16.8	84.0	1056	10	10	US-09-899-575-16	Sequence 16, Appl
c 42	16.8	84.0	1780	14	14	US-10-164-278-13	Sequence 13, Appl
c 43	16.8	84.0	1780	22	22	US-10-164-278-13	Sequence 13, Appl
c 44	16.8	84.0	1780	22	22	US-10-449-370-3	Sequence 3, Appli
c 45	16.8	84.0	1824	17	17	US-10-386-414-9	Sequence 9, Appli

Result		Query					Description
No.	Score	Match	Length	DB	ID		
C	1	20	100.0	1522	4	US-09-949-016-1695	Sequence 1695, Ap
C	2	20	100.0	2343	2	US-09-018-760-3	Sequence 3, Appli
C	3	20	100.0	3016	4	US-09-023-655-259	Sequence 259, App
C	4	20	100.0	17353	4	US-09-949-016-13437	Sequence 13437, A
C	5	18.4	92.0	228	4	US-09-513-999C-14175	Sequence 14175, A
C	6	18.4	92.0	1414	4	US-09-949-016-2364	Sequence 2364, Ap
C	7	18.4	92.0	7158	4	US-09-949-016-14106	Sequence 14106, A
	8	18	90.0	601	4	US-09-949-016-58445	Sequence 58445, A
C	9	16.8	84.0	177	4	US-09-536-977-31	Sequence 31, Appl
C	10	16.8	84.0	258	3	US-09-109-204-22	Sequence 22, Appl
C	11	16.8	84.0	258	4	US-09-490-032-22	Sequence 22, Appl

c	12	16.8	84.0	432	4	US-09-536-977-53	Sequence 53, Appl
c	13	16.8	84.0	434	4	US-09-536-977-55	Sequence 55, Appl
c	14	16.8	84.0	798	4	US-09-536-977-61	Sequence 61, Appl
c	15	16.8	84.0	800	4	US-09-536-977-63	Sequence 63, Appl
c	16	16.8	84.0	1038	4	US-09-536-977-75	Sequence 75, Appl
c	17	16.8	84.0	2071	4	US-09-536-977-69	Sequence 69, Appl
c	18	16.8	84.0	2181	4	US-09-475-515-58	Sequence 58, Appl
c	19	16.8	84.0	2224	3	US-09-109-204-6	Sequence 6, Appli
c	20	16.8	84.0	2224	4	US-09-490-032-6	Sequence 6, Appli
c	21	16.8	84.0	2298	4	US-09-476-242-22	Sequence 22, Appl
c	22	16.8	84.0	2298	4	US-09-476-242-23	Sequence 23, Appl
c	23	16.8	84.0	2298	4	US-09-476-242-24	Sequence 24, Appl
c	24	16.8	84.0	2310	4	US-09-476-242-3	Sequence 3, Appli
c	25	16.8	84.0	2310	4	US-09-476-242-21	Sequence 21, Appl
c	26	16.8	84.0	2316	4	US-09-476-242-4	Sequence 4, Appli
c	27	16.8	84.0	2316	4	US-09-476-242-8	Sequence 8, Appli
c	28	16.8	84.0	2322	4	US-09-476-242-5	Sequence 5, Appli
c	29	16.8	84.0	2322	4	US-09-476-242-18	Sequence 18, Appl
c	30	16.8	84.0	2322	4	US-09-476-242-19	Sequence 19, Appl
c	31	16.8	84.0	2322	4	US-09-476-242-20	Sequence 20, Appl
c	32	16.8	84.0	2328	4	US-09-476-242-6	Sequence 6, Appli
c	33	16.8	84.0	2334	4	US-09-476-242-7	Sequence 7, Appli
c	34	16.8	84.0	2340	4	US-09-475-515-67	Sequence 67, Appl
c	35	16.8	84.0	2352	4	US-09-476-242-26	Sequence 26, Appl
c	36	16.8	84.0	2358	4	US-09-475-515-50	Sequence 50, Appl
c	37	16.8	84.0	2358	4	US-09-476-242-25	Sequence 25, Appl
c	38	16.8	84.0	2385	4	US-09-475-515-68	Sequence 68, Appl
c	39	16.8	84.0	2466	4	US-09-475-515-49	Sequence 49, Appl
c	40	16.8	84.0	2469	4	US-09-536-977-71	Sequence 71, Appl
c	41	16.8	84.0	2517	4	US-09-476-242-16	Sequence 16, Appl
c	42	16.8	84.0	2517	4	US-09-476-242-17	Sequence 17, Appl
c	43	16.8	84.0	2523	4	US-09-476-242-15	Sequence 15, Appl
c	44	16.8	84.0	2529	4	US-09-476-242-14	Sequence 14, Appl
c	45	16.8	84.0	2535	4	US-09-476-242-13	Sequence 13, Appl

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OM nucleic - nucleic search, using sw model

Run on: October 11, 2005, 06:09:23 ; Search time 17.7647 Seconds
(without alignments)
6664.609 Million cell updates/sec

Title: US-10-798-678-10
Perfect score: 20
Sequence: 1 cagcccacgggtcatgatgaa 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	20	100.0	20	13	ADS13181	Ads13181 PCR prime
2	20	100.0	21	2	AAV01296	Aav01296 Creatine
c 3	20	100.0	398	9	ACH17818	Ach17818 Human adu
c 4	20	100.0	419	9	ACH17947	Ach17947 Human adu

c	5	20	100.0	1146	2	AAQ86990	Aaq86990 Creatine-
c	6	20	100.0	1437	3	AAF18037	Aaf18037 Lung canc
c	7	20	100.0	1548	12	ADQ86954	Adq86954 Human tum
c	8	20	100.0	1562	6	AAD27212	Aad27212 Human AAA
c	9	20	100.0	1563	4	AAH23099	Aah23099 Osteoarth
c	10	20	100.0	1568	2	AAQ58990	Aaq58990 Mutant hu
c	11	20	100.0	1568	2	AAQ51620	Aaq51620 Human cre
c	12	20	100.0	1620	10	ADF09662	Adf09662 Human MAP
c	13	20	100.0	2343	2	AAX99989	Aax99989 Creatine
c	14	20	100.0	3016	11	ADI30933	Adi30933 Human cDN
c	15	18.4	92.0	228	3	AAC10100	Aac10100 Human sec
c	16	18.4	92.0	452	9	ACH39210	Ach39210 Human foe
c	17	18.4	92.0	574	12	ADQ92076	Adq92076 Human aut
c	18	18.4	92.0	665	2	AAQ05829	Aaq05829 Human B i
c	19	18.4	92.0	1024	10	ABZ83251	Abz83251 Toxicolog
c	20	18.4	92.0	1146	2	AAQ86989	Aaq86989 Creatine-
c	21	18.4	92.0	1355	13	ACN39756	Acn39756 Tumour-as
c	22	18.4	92.0	1360	6	ABL62370	Abl62370 Colon ade
c	23	18.4	92.0	1360	6	ABN95771	Abn95771 Gene #226
c	24	18.4	92.0	1376	2	AAQ51619	Aaq51619 Human cre
	25	18.4	92.0	1390	6	ABQ54381	Abq54381 Human ova
c	26	18.4	92.0	1432	12	ADP10454	Adp10454 Reference
c	27	18.4	92.0	1432	13	ADR14270	Adr14270 Human NF-
c	28	18.4	92.0	1589	3	AAA64203	Aaa64203 cDNA sequ
c	29	17	85.0	378	8	ABX36794	Abx36794 Bovine ES
c	30	17	85.0	381	8	ABX41804	Abx41804 Bovine ES
c	31	17	85.0	408	8	ABX44384	Abx44384 Bovine ES
c	32	17	85.0	996	6	ABN74412	Abn74412 Bovine em
c	33	16.8	84.0	177	3	AAA49075	Aaa49075 Snut 1890
c	34	16.8	84.0	258	3	AAZ46040	Aaz46040 Partial c
c	35	16.8	84.0	434	3	AAA49087	Aaa49087 Piece 4gp
c	36	16.8	84.0	798	3	AAA49090	Aaa49090 Piece 8gp
c	37	16.8	84.0	800	3	AAA49091	Aaa49091 Piece 8gp
	38	16.8	84.0	804	10	ACF71304	Acf71304 Photorhab
c	39	16.8	84.0	843	10	ADD47227	Add47227 Rat gene
c	40	16.8	84.0	1035	3	AAA51616	Aaa51616 HIV gp41
c	41	16.8	84.0	1038	3	AAA49097	Aaa49097 synBX08-
c	42	16.8	84.0	1056	3	AAA51623	Aaa51623 HIV gp41
c	43	16.8	84.0	1780	8	ABZ23175	Abz23175 Polynucle
c	44	16.8	84.0	1780	12	ADF11374	Adf11374 Human CAR
c	45	16.8	84.0	1824	6	ABK87939	Abk87939 Human arg

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OM nucleic - nucleic search, using sw model

Run on: October 11, 2005, 06:09:23 ; Search time 96.0654 Seconds
(without alignments)
10087.968 Million cell updates/sec

Title: US-10-798-678-10
Perfect score: 20
Sequence: 1 cagccccacgggtcatgatgaa 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query					Description
	No.	Score	Match Length	DB	ID	
	1	20	100.0	21	11 DOGCKMB	L77481 Canis famil
c	2	20	100.0	242	9 HUMCKMM3	M21489 Human muscl
c	3	20	100.0	819	4 AF130753	AF130753 Equus cab

c	4	20	100.0	915	5	AY130384	AY130384 Petromyzo
c	5	20	100.0	1143	6	BD062320	BD062320 Solution-
c	6	20	100.0	1146	4	AF120106	AF120106 Bos tauru
c	7	20	100.0	1146	5	AB118942	AB118942 Lethenter
c	8	20	100.0	1146	9	BT006793	BT006793 Homo sapi
c	9	20	100.0	1146	12	AY335559	AY335559 Synthetic
c	10	20	100.0	1146	12	BT007908	BT007908 Synthetic
c	11	20	100.0	1338	5	AB103475	AB103475 Lethenter
c	12	20	100.0	1342	4	RABCKB	M11306 Rabbit crea
c	13	20	100.0	1428	5	FSCCKPA	M36427 T.californi
c	14	20	100.0	1434	5	FSCCK	M11508 T.marmorata
c	15	20	100.0	1465	4	RABCPK	K02831 Rabbit musc
c	16	20	100.0	1521	6	CQ719881	CQ719881 Sequence
c	17	20	100.0	1527	4	DOGCK	M11660 Dog cardiac
c	18	20	100.0	1555	9	AK129878	AK129878 Homo sapi
c	19	20	100.0	1562	6	AX322770	AX322770 Sequence
c	20	20	100.0	1562	9	HUMCKMA	M14780 Human creat
c	21	20	100.0	1563	6	AX202099	AX202099 Sequence
c	22	20	100.0	1619	9	BC007462	BC007462 Homo sapi
c	23	20	100.0	2343	6	AR084972	AR084972 Sequence
c	24	20	100.0	3016	6	AR379714	AR379714 Sequence
c	25	20	100.0	20454	9	AY585238	AY585238 Homo sapi
	26	20	100.0	44052	9	AC005781	AC005781 Homo sapi
	27	20	100.0	155060	2	AC140158	AC140158 Felis cat
	28	20	100.0	156383	2	AC135221	AC135221 Felis cat
	29	20	100.0	160069	2	AC023329	AC023329 Homo sapi
	30	20	100.0	163038	2	AC135542	AC135542 Pan trogl
	31	20	100.0	173728	2	AC139878	AC139878 Sus scrof
	32	20	100.0	197005	2	AC137535	AC137535 Bos tauru
	33	20	100.0	199160	2	AC137538	AC137538 Canis fam
c	34	18.4	92.0	108	9	HUMCKB3	M22356 Human creat
c	35	18.4	92.0	210	9	HUMCKBB3	M21238 Human creat
c	36	18.4	92.0	228	6	AX898312	AX898312 Sequence
c	37	18.4	92.0	228	6	BD033845	BD033845 Sequence
c	38	18.4	92.0	540	3	AY608673	AY608673 Branchios
c	39	18.4	92.0	574	6	CQ832393	CQ832393 Sequence
c	40	18.4	92.0	916	5	AY130383	AY130383 Myxine gl
c	41	18.4	92.0	1137	3	AF251440	AF251440 Branchios
c	42	18.4	92.0	1143	6	BD062321	BD062321 Solution-
c	43	18.4	92.0	1146	5	AB118943	AB118943 Lethenter
c	44	18.4	92.0	1146	9	CR542268	CR542268 Homo sapi
c	45	18.4	92.0	1146	12	AY335755	AY335755 Synthetic

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OM nucleic - nucleic search, using sw model

Run on: October 11, 2005, 06:09:23 ; Search time 151.32 Seconds
(without alignments)
5030.955 Million cell updates/sec

Title: US-10-798-678-9
Perfect score: 20
Sequence: 1 tctgacccagaggtgtcaag 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Match	Length	DB	ID	Description
No.		%					
1	18.4	92.0	496	9	BX981645		BX981645 Forward s
2	18.4	92.0	600	9	CR048849		CR048849 Reverse s
3	18.4	92.0	627	9	CR070097		CR070097 Reverse s
4	18.4	92.0	630	9	CR113345		CR113345 Reverse s
c 5	17.4	87.0	127	1	AA452683		AA452683 zx39a02.r
c 6	17.4	87.0	374	4	BI299618		BI299618 UI-R-CV2-
c 7	17.4	87.0	375	7	CO908555		CO908555 BJ02032C1
c 8	17.4	87.0	375	7	CR465162		CR465162 CR465162

c	9	17.4	87.0	420	4	BI300554	BI300554 UI-R-CV2-
	10	17.4	87.0	469	7	CV358207	CV358207 MR4-UT009
c	11	17.4	87.0	484	4	BG373108	BG373108 UI-R-CV1-
c	12	17.4	87.0	532	5	BQ201241	BQ201241 UI-R-DQ1-
	13	17.4	87.0	549	7	CF107151	CF107151 Shultzomi
	14	17.4	87.0	567	7	W93695	W93695 zd96b06.s1
c	15	17.4	87.0	658	4	BI291457	BI291457 UI-R-CV2-
	16	17.4	87.0	1234	9	CL649766	CL649766 CH213-250
c	17	17	85.0	194	8	B86217	B86217 RPCI11-22G1
c	18	17	85.0	360	8	AQ009084	AQ009084 RPCI11-22
c	19	17	85.0	558	1	AA703244	AA703244 zi70e08.s
	20	17	85.0	676	9	AG152590	AG152590 Pan trogl
c	21	16.8	84.0	217	8	AZ818229	AZ818229 2M0088E09
c	22	16.8	84.0	343	7	CK703751	CK703751 ZF101-P00
c	23	16.8	84.0	381	6	CD537225	CD537225 NcEST3b74
c	24	16.8	84.0	421	8	AQ371437	AQ371437 HS_5043_A
c	25	16.8	84.0	477	8	AZ269170	AZ269170 RPCI-23-1
c	26	16.8	84.0	488	6	CB882376	CB882376 HL01L04w
	27	16.8	84.0	499	6	BY569812	BY569812 BY569812
	28	16.8	84.0	518	1	AA834244	AA834244 of16e05.s
c	29	16.8	84.0	538	5	BQ101582	BQ101582 ih93b02.y
	30	16.8	84.0	539	5	BQ101318	BQ101318 ih93b02.x
c	31	16.8	84.0	589	8	AZ121127	AZ121127 RPCI-23-1
	32	16.8	84.0	601	4	BJ455315	BJ455315 BJ455315
	33	16.8	84.0	602	9	CR841899	CR841899 GR0AAA76B
c	34	16.8	84.0	633	8	AZ817596	AZ817596 2M0087H12
c	35	16.8	84.0	648	8	BH026363	BH026363 RPCI-24-2
c	36	16.8	84.0	648	9	CR223530	CR223530 Forward s
c	37	16.8	84.0	686	9	CR211404	CR211404 Forward s
c	38	16.8	84.0	696	7	CN463121	CN463121 6123.1 Af
c	39	16.8	84.0	700	8	BZ142687	BZ142687 CH230-318
c	40	16.8	84.0	721	9	CR012945	CR012945 Forward s
c	41	16.8	84.0	740	9	AG604192	AG604192 Mus muscu
c	42	16.8	84.0	755	2	BE513483	BE513483 601316176
c	43	16.8	84.0	767	9	CC543607	CC543607 CH240_425
c	44	16.8	84.0	773	9	AG506946	AG506946 Mus muscu
	45	16.8	84.0	805	8	BH096053	BH096053 RPCI-24-2

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OM nucleic - nucleic search, using sw model

Run on: October 11, 2005, 06:09:25 ; Search time 57.5948 Seconds
(without alignments)
2418.567 Million cell updates/sec

Title: US-10-798-678-9
Perfect score: 20
Sequence: 1 tctgacccagaggtgtcaag 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 8443130 seqs, 3482420727 residues

Total number of hits satisfying chosen parameters: 16886260

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:*
- 22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%	Query					
No.	Score	Match	Length	DB	ID	Description		
1	20	100.0	20	20	US-10-798-678-9	Sequence 9, Appli		
2	20	100.0	1115	20	US-10-798-678-2	Sequence 2, Appli		
c 3	17	85.0	577	13	US-10-027-632-134960	Sequence 134960,		
c 4	17	85.0	577	17	US-10-027-632-134960	Sequence 134960,		
c 5	17	85.0	2593	19	US-10-676-248B-23	Sequence 23, Appl		
6	17	85.0	136726	17	US-10-085-117-244	Sequence 244, App		
c 7	16.8	84.0	477	13	US-10-027-632-47629	Sequence 47629, A		
c 8	16.8	84.0	477	17	US-10-027-632-47629	Sequence 47629, A		
c 9	16.8	84.0	562	19	US-10-437-963-19546	Sequence 19546, A		
c 10	16.8	84.0	623	13	US-10-027-632-82259	Sequence 82259, A		
c 11	16.8	84.0	623	13	US-10-027-632-109818	Sequence 109818,		
c 12	16.8	84.0	623	17	US-10-027-632-82259	Sequence 82259, A		
c 13	16.8	84.0	623	17	US-10-027-632-109818	Sequence 109818,		
14	16.8	84.0	679	13	US-10-027-632-102119	Sequence 102119,		
15	16.8	84.0	679	13	US-10-027-632-102120	Sequence 102120,		
16	16.8	84.0	679	17	US-10-027-632-102119	Sequence 102119,		
17	16.8	84.0	679	17	US-10-027-632-102120	Sequence 102120,		
c 18	16.8	84.0	227448	21	US-10-461-862-53	Sequence 53, Appl		
c 19	15.8	79.0	25	21	US-10-719-900-652290	Sequence 652290,		
20	15.8	79.0	436	9	US-09-981-876-18	Sequence 18, Appl		
21	15.8	79.0	436	10	US-09-148-545-18	Sequence 18, Appl		
22	15.8	79.0	436	22	US-10-979-111-18	Sequence 18, Appl		
c 23	15.8	79.0	480	10	US-09-918-995-25562	Sequence 25562, A		
c 24	15.8	79.0	543	13	US-10-027-632-11875	Sequence 11875, A		
c 25	15.8	79.0	543	17	US-10-027-632-11875	Sequence 11875, A		
c 26	15.8	79.0	925	20	US-10-425-115-1741	Sequence 1741, Ap		
27	15.8	79.0	977	17	US-10-264-237-772	Sequence 772, App		
28	15.8	79.0	1177	17	US-10-013-312-2986	Sequence 2986, Ap		
29	15.8	79.0	1315	17	US-10-131-410-61	Sequence 61, Appl		
30	15.8	79.0	1686	9	US-09-938-842A-564	Sequence 564, App		
31	15.8	79.0	1686	11	US-09-938-842A-564	Sequence 564, App		
32	15.8	79.0	1686	24	US-11-069-633-1	Sequence 1, Appli		
33	15.8	79.0	1726	9	US-09-917-800A-1346	Sequence 1346, Ap		
34	15.8	79.0	1726	17	US-10-388-934-158	Sequence 158, App		
35	15.8	79.0	1726	18	US-10-152-319A-1855	Sequence 1855, Ap		
36	15.8	79.0	1833	22	US-10-450-763-3325	Sequence 3325, Ap		
37	15.8	79.0	2100	10	US-09-809-391-171	Sequence 171, App		
38	15.8	79.0	2100	10	US-09-882-171-171	Sequence 171, App		
39	15.8	79.0	2100	17	US-10-164-861-171	Sequence 171, App		
40	15.8	79.0	2186	17	US-10-104-047-46	Sequence 46, Appl		
41	15.8	79.0	2617	17	US-10-013-312-1314	Sequence 1314, Ap		
42	15.8	79.0	2617	19	US-10-313-972-22	Sequence 22, Appl		
43	15.8	79.0	2617	19	US-10-313-972-105	Sequence 105, App		
44	15.8	79.0	2619	19	US-10-313-972-106	Sequence 106, App		
45	15.8	79.0	2619	19	US-10-313-972-107	Sequence 107, App		

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	17.4	87.0	36227	4	US-09-949-016-13951	Sequence 13951, A
2	17	85.0	120727	4	US-09-949-016-15787	Sequence 15787, A
3	17	85.0	120727	4	US-09-949-016-15788	Sequence 15788, A
4	15.8	79.0	436	4	US-09-148-545-18	Sequence 18, Appl
5	15.8	79.0	2100	3	US-09-149-476-171	Sequence 171, App
6	15.8	79.0	14494	4	US-09-949-016-2005	Sequence 2005, Ap
C 7	15.8	79.0	97195	4	US-09-949-016-12212	Sequence 12212, A
C 8	15.8	79.0	97196	4	US-09-949-016-16971	Sequence 16971, A
9	15.8	79.0	198942	4	US-09-949-016-13209	Sequence 13209, A
10	15.4	77.0	28555	4	US-09-949-016-13106	Sequence 13106, A
C 11	15.4	77.0	36180	4	US-09-949-016-11745	Sequence 11745, A

c	12	15.4	77.0	36181	4	US-09-949-016-16163	Sequence 16163, A
c	13	15.4	77.0	36741	3	US-09-301-665-3	Sequence 3, Appli
	14	15.2	76.0	441	4	US-09-270-767-2128	Sequence 2128, Ap
	15	15.2	76.0	441	4	US-09-270-767-17410	Sequence 17410, A
	16	15.2	76.0	601	4	US-09-949-016-155554	Sequence 155554,
	17	15.2	76.0	601	4	US-09-949-016-155555	Sequence 155555,
	18	15.2	76.0	601	4	US-09-949-016-155653	Sequence 155653,
	19	15.2	76.0	601	4	US-09-949-016-155654	Sequence 155654,
	20	15.2	76.0	601	4	US-09-949-016-174957	Sequence 174957,
c	21	15.2	76.0	4491	4	US-09-673-429-1	Sequence 1, Appli
	22	15.2	76.0	12707	4	US-09-949-016-14243	Sequence 14243, A
	23	15.2	76.0	12707	4	US-09-949-016-14244	Sequence 14244, A
	24	15.2	76.0	16455	4	US-09-949-016-14292	Sequence 14292, A
	25	15.2	76.0	16470	4	US-09-949-016-14401	Sequence 14401, A
	26	15.2	76.0	20922	4	US-09-949-016-14335	Sequence 14335, A
	27	15.2	76.0	24913	4	US-09-949-016-11889	Sequence 11889, A
c	28	15.2	76.0	43577	4	US-09-949-016-16694	Sequence 16694, A
	29	15.2	76.0	49931	4	US-09-949-016-13727	Sequence 13727, A
	30	15.2	76.0	49931	4	US-09-949-016-13728	Sequence 13728, A
	31	15.2	76.0	49931	4	US-09-949-016-13729	Sequence 13729, A
	32	15.2	76.0	93971	4	US-09-949-016-16097	Sequence 16097, A
	33	15.2	76.0	93971	4	US-09-949-016-16098	Sequence 16098, A
	34	15.2	76.0	100848	4	US-09-596-002-39	Sequence 39, Appl
	35	15.2	76.0	181251	4	US-09-949-016-15970	Sequence 15970, A
c	36	15.2	76.0	236474	4	US-09-949-016-13418	Sequence 13418, A
c	37	15.2	76.0	237241	4	US-09-949-016-16101	Sequence 16101, A
c	38	15.2	76.0	239527	4	US-09-949-016-15980	Sequence 15980, A
	39	15	75.0	601	4	US-09-949-016-138601	Sequence 138601,
	40	15	75.0	9275	4	US-09-949-016-15651	Sequence 15651, A
c	41	14.8	74.0	428	4	US-09-702-705-270	Sequence 270, App
c	42	14.8	74.0	428	4	US-09-736-457-270	Sequence 270, App
c	43	14.8	74.0	428	4	US-09-614-124B-270	Sequence 270, App
c	44	14.8	74.0	428	4	US-09-671-325-270	Sequence 270, App
c	45	14.8	74.0	428	4	US-09-589-184-270	Sequence 270, App

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OM nucleic - nucleic search, using sw model

Run on: October 11, 2005, 06:09:23 ; Search time 17.7647 Seconds
(without alignments)
6664.609 Million cell updates/sec

Title: US-10-798-678-9
Perfect score: 20
Sequence: 1 tctgacccagaggtgtcaag 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	20	100.0	20	13	ADS13180	Ads13180 PCR prime
2	20	100.0	1115	13	ADS13173	Ads13173 Porcine c
c 3	17	85.0	2593	12	ADM18399	Adm18399 Human chr
c 4	16.8	84.0	227448	13	ABD32841	Abd32841 Mouse can

c	5	16	80.0	31337	12	ADQ97031	Adq97031 Mouse can
	6	15.8	79.0	436	2	AAV34161	Aav34161 Human sec
	7	15.8	79.0	436	8	ACD08032	Acd08032 cDNA enco
c	8	15.8	79.0	480	9	ACH38350	Ach38350 Human end
	9	15.8	79.0	687	4	AAH03613	Aah03613 Human cDN
	10	15.8	79.0	690	4	AAD05618	Aad05618 Human sec
	11	15.8	79.0	801	2	AAZ15109	Aaz15109 Human gen
	12	15.8	79.0	977	6	ABL90210	Abl90210 Human pol
	13	15.8	79.0	1315	2	AAZ33668	Aaz33668 Human bre
	14	15.8	79.0	1686	6	ABZ12759	Abz12759 Arabidops
	15	15.8	79.0	1726	6	ABK63439	Abk63439 Rat seque
	16	15.8	79.0	1726	10	ADB57851	Adb57851 Toxicity-
	17	15.8	79.0	1726	10	ADB53162	Adb53162 Primary r
	18	15.8	79.0	1726	10	ABT42153	Abt42153 Toxicity
	19	15.8	79.0	1833	5	AAS67521	Aas67521 DNA encod
	20	15.8	79.0	1923	10	ADD96984	Add96984 Human 193
	21	15.8	79.0	2100	2	AAV59671	Aav59671 Human sec
	22	15.8	79.0	2100	6	ABS73658	Abs73658 Human cDN
	23	15.8	79.0	2100	9	ACD82801	Acd82801 cDNA sequ
	24	15.8	79.0	2100	10	ADI22886	Adi22886 cDNA enco
	25	15.8	79.0	2100	12	ADH73888	Adh73888 Human sec
	26	15.8	79.0	2100	12	ADL83022	Adl83022 Human PRO
	27	15.8	79.0	2100	12	ADN05917	Adn05917 Antipsori
	28	15.8	79.0	2108	4	AAH13789	Aah13789 Human cDN
c	29	15.8	79.0	2173	4	AAI59603	Aai59603 Human pol
c	30	15.8	79.0	2173	4	AAI59604	Aai59604 Human pol
	31	15.8	79.0	2186	10	ADB61892	Adb61892 Human cDN
	32	15.8	79.0	2508	10	ADF82086	Adf82086 Leukaemia
	33	15.8	79.0	2617	10	ADD96991	Add96991 Human 193
	34	15.8	79.0	2617	10	ADD96907	Add96907 Human 193
	35	15.8	79.0	2617	10	ADD96989	Add96989 Human 193
	36	15.8	79.0	2617	12	ADP49706	Adp49706 Human 193
	37	15.8	79.0	2617	12	ADP49789	Adp49789 Human 193
	38	15.8	79.0	2617	12	ADP49790	Adp49790 Human 193
	39	15.8	79.0	2618	12	ADP49791	Adp49791 Human 193
	40	15.8	79.0	2653	4	AAH14004	Aah14004 Human cDN
	41	15.8	79.0	2653	6	AAD45690	Aad45690 Human LBD
	42	15.8	79.0	2669	13	ADS09994	Ads09994 Human the
	43	15.8	79.0	2679	10	ADD96905	Add96905 Human 193
	44	15.8	79.0	2679	10	ADD96983	Add96983 Human 193
	45	15.8	79.0	2679	10	ADD96985	Add96985 Human 193

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OM nucleic - nucleic search, using sw model

Run on: October 11, 2005, 06:09:23 ; Search time 96.0654 Seconds
(without alignments)
10087.968 Million cell updates/sec

Title: US-10-798-678-9
Perfect score: 20
Sequence: 1 tctgacccagaggtgtcaag 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query		DB	ID	Description
			Match	Length			
c	1	20	100.0	173728	2	AC139878	AC139878 Sus scrof
c	2	18.4	92.0	184890	2	AC102608	AC102608 Mus muscu
	3	18.4	92.0	210372	10	AC122807	AC122807 Mus muscu

	4	18.4	92.0	224766	2	AC132138	AC132138 Mus muscu
	5	18.4	92.0	225265	2	AC095890	AC095890 Rattus no
	6	18.4	92.0	240020	2	AC127821	AC127821 Rattus no
c	7	18	90.0	139520	5	AL935199	AL935199 Zebrafish
	8	18	90.0	186097	2	CR735102	CR735102 Danio rer
c	9	17.4	87.0	1479	11	BV176732	BV176732 sqnm90601
c	10	17.4	87.0	1479	11	BV177548	BV177548 sqnm95313
c	11	17.4	87.0	1479	11	BV178088	BV178088 sqnm98482
	12	17.4	87.0	2693	1	AY187681	AY187681 Vibrio vu
c	13	17.4	87.0	89000	9	AC016932	AC016932 Homo sapi
c	14	17.4	87.0	110000	2	BX640582_4	Continuation (5 of
	15	17.4	87.0	128614	10	BX510300	BX510300 Mouse DNA
	16	17.4	87.0	130699	5	BX571796	BX571796 Zebrafish
c	17	17.4	87.0	161492	9	AC007780	AC007780 Homo sapi
	18	17.4	87.0	204008	2	AC094417	AC094417 Rattus no
c	19	17.4	87.0	234633	2	AC111768	AC111768 Rattus no
c	20	17.4	87.0	248650	1	AP005341	AP005341 Vibrio vu
c	21	17.4	87.0	261688	2	AC111685	AC111685 Rattus no
c	22	17.4	87.0	269607	2	AC096303	AC096303 Rattus no
c	23	17.4	87.0	271135	2	AC105492	AC105492 Rattus no
	24	17.4	87.0	272030	2	AC105482	AC105482 Rattus no
c	25	17	85.0	10026	1	AE013961	AE013961 Yersinia
c	26	17	85.0	110000	1	BX936398_41	Continuation (42 o
	27	17	85.0	111051	2	AF322449	AF322449 Homo sapi
	28	17	85.0	148456	2	AL133550	AL133550 Homo sapi
c	29	17	85.0	166238	2	AC019280	AC019280 Homo sapi
	30	17	85.0	168528	9	AL355861	AL355861 Human DNA
	31	17	85.0	169405	9	AC092800	AC092800 Homo sapi
c	32	17	85.0	183218	10	AC132440	AC132440 Mus muscu
c	33	17	85.0	200033	9	HSA251973	AJ251973 Homo sapi
	34	17	85.0	201050	1	AJ414143	AJ414143 Yersinia
c	35	17	85.0	207661	9	AC015884	AC015884 Homo sapi
	36	17	85.0	215041	2	AC119025	AC119025 Rattus no
	37	17	85.0	224955	2	AC125710	AC125710 Rattus no
	38	17	85.0	290924	1	AE017138	AE017138 Yersinia
c	39	16.8	84.0	12978	9	AC025732	AC025732 Homo sapi
c	40	16.8	84.0	30946	9	HSU230G7	Z97355 Human DNA s
	41	16.8	84.0	44312	9	AB065453	AB065453 Homo sapi
c	42	16.8	84.0	57994	2	AC084181	AC084181 Homo sapi
	43	16.8	84.0	70231	5	AC092870	AC092870 Takifugu
c	44	16.8	84.0	76727	9	HS821D11	AL021453 Human DNA
c	45	16.8	84.0	82654	9	AL353713	AL353713 Human DNA

OM nucleic - nucleic search, using sw model

Result	No.	Score	%		DB	ID	Description
			Query	Match			
C	1	24.4	59.5	236	2	AW430539	AW430539 70203 MAR
	2	24.4	59.5	468	6	CD740207	CD740207 4029011 1
	3	23	56.1	304	2	AW806395	AW806395 MR4-UM011
C	4	23	56.1	592	4	BJ612701	BJ612701 BJ612701
	5	22.8	55.6	460	2	BF074053	BF074053 221374 MA
	6	22.8	55.6	558	2	AW658841	AW658841 95621 MAR
	7	22.8	55.6	569	1	AV607653	AV607653 AV607653
	8	22.8	55.6	610	2	BF064541	BF064541 HV CEB001

	9	22.8	55.6	790	7	CK193867	CK193867 FGAS00228
	10	22.6	55.1	337	2	BE327239	BE327239 hw09b12.x
	11	22.6	55.1	619	9	FR0005482	Z89292 F.rubripes
c	12	22.6	55.1	619	9	FR0005502	Z89312 F.rubripes
c	13	22.6	55.1	659	1	AL869073	AL869073 AL869073
c	14	22.4	54.6	411	4	BF958189	BF958189 PM4-NN120
	15	22.4	54.6	566	9	CE636394	CE636394 tigr-gss-
	16	22.4	54.6	654	9	CE024016	CE024016 tigr-gss-
c	17	22.2	54.1	592	9	FR0040022	AL127516 Fugu rubr
	18	22.2	54.1	698	1	AI225616	AI225616 uj13e05.y
c	19	22.2	54.1	770	9	AG587982	AG587982 Mus muscu
	20	22.2	54.1	955	9	CNS02R9L	AL210306 Tetraodon
c	21	22	53.7	262	7	R09009	R09009 yf25c02.r1
	22	22	53.7	352	2	BE047684	BE047684 tz40e10.y
c	23	22	53.7	462	6	CA703558	CA703558 wdk1c.pk0
c	24	22	53.7	556	4	BJ207889	BJ207889 BJ207889
c	25	22	53.7	563	6	CD320553	CD320553 StrPu538.
c	26	22	53.7	593	4	BJ281245	BJ281245 BJ281245
c	27	22	53.7	596	1	AL825702	AL825702 AL825702
	28	22	53.7	616	4	BJ215174	BJ215174 BJ215174
	29	22	53.7	631	4	BJ253710	BJ253710 BJ253710
	30	22	53.7	634	6	CD866509	CD866509 AZO2.103K
	31	22	53.7	640	9	CR841913	CR841913 GR0AAA76B
c	32	22	53.7	654	4	BJ247616	BJ247616 BJ247616
	33	22	53.7	664	4	BJ284049	BJ284049 BJ284049
c	34	22	53.7	667	4	BJ278995	BJ278995 BJ278995
c	35	22	53.7	670	6	CD920693	CD920693 G608.118B
c	36	22	53.7	691	6	CD291537	CD291537 StrPu538.
	37	22	53.7	705	4	BJ286306	BJ286306 BJ286306
c	38	22	53.7	705	6	CD866532	CD866532 AZO2.103L
	39	22	53.7	760	6	CB675289	CB675289 OSJNEe100
c	40	22	53.7	814	7	CK200687	CK200687 FGAS00920
	41	22	53.7	831	7	CO479347	CO479347 GQ018M01.
	42	22	53.7	1043	4	BM457152	BM457152 AGENCOURT
	43	22	53.7	1124	7	CK212024	CK212024 FGAS02388
c	44	21.8	53.2	302	2	BB607242	BB607242 BB607242
	45	21.8	53.2	456	6	CA619735	CA619735 w11n.pk00

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OM nucleic - nucleic search, using sw model

Run on: October 11, 2005, 06:09:25 ; Search time 118.069 Seconds
(without alignments)
2418.567 Million cell updates/sec

Title: US-10-798-678-12
Perfect score: 41
Sequence: 1 atcatgcgcttcaccgactg.....gagaaagagcctctccgtcc 41

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 8443130 seqs, 3482420727 residues

Total number of hits satisfying chosen parameters: 16886260

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:*
- 22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				
No.	Score	Query	Match	Length	DB	ID	Description
	1	41	100.0	41	20	US-10-798-678-12	Sequence 12, Appl
c	2	24	58.5	1115	20	US-10-798-678-2	Sequence 2, Appli
	3	22.6	55.1	11987	10	US-09-764-891-9972	Sequence 9972, Ap
c	4	22	53.7	671	20	US-10-425-115-5746	Sequence 5746, Ap
c	5	22	53.7	3063	22	US-10-756-149-2625	Sequence 2625, Ap
c	6	21.6	52.7	504	16	US-10-029-386-8027	Sequence 8027, Ap
	7	21.4	52.2	2871	19	US-10-437-963-19391	Sequence 19391, A
c	8	21.2	51.7	1415	20	US-10-739-930-2017	Sequence 2017, Ap
c	9	21	51.2	339	20	US-10-425-115-26072	Sequence 26072, A
	10	20.8	50.7	340	18	US-10-424-599-46323	Sequence 46323, A
c	11	20.8	50.7	600	22	US-10-972-079-48666	Sequence 48666, A
c	12	20.8	50.7	3401	17	US-10-320-797-126	Sequence 126, App
	13	20.6	50.2	462	24	US-11-097-143-39443	Sequence 39443, A
	14	20.6	50.2	1365	24	US-11-097-143-35870	Sequence 35870, A
c	15	20.6	50.2	1612	18	US-10-425-114-22343	Sequence 22343, A
c	16	20.6	50.2	1900	19	US-10-437-963-26566	Sequence 26566, A
c	17	20.6	50.2	3464	24	US-11-097-143-35869	Sequence 35869, A
c	18	20.6	50.2	3759	24	US-11-097-143-5867	Sequence 5867, Ap
	19	20.6	50.2	4510	24	US-11-097-143-39442	Sequence 39442, A
c	20	20.6	50.2	6020	24	US-11-097-143-5866	Sequence 5866, Ap
	21	20.6	50.2	147309	9	US-09-742-312-3	Sequence 3, Appli
	22	20.6	50.2	147309	16	US-10-436-185-3	Sequence 3, Appli
	23	20.4	49.8	1827	20	US-10-411-910A-211	Sequence 211, App
	24	20.4	49.8	304905	18	US-10-271-416-1	Sequence 1, Appli
	25	20.2	49.3	257	19	US-10-430-201-89	Sequence 89, Appl
	26	20.2	49.3	257	19	US-10-430-201-90	Sequence 90, Appl
	27	20.2	49.3	354	20	US-10-425-115-113315	Sequence 113315,
	28	20.2	49.3	469	17	US-10-242-535A-38567	Sequence 38567, A
	29	20.2	49.3	469	18	US-10-085-783A-38567	Sequence 38567, A
	30	20.2	49.3	585	21	US-10-489-864-4	Sequence 4, Appli
c	31	20.2	49.3	600	22	US-10-972-079-52002	Sequence 52002, A
c	32	20.2	49.3	600	22	US-10-972-079-52003	Sequence 52003, A
c	33	20.2	49.3	614	10	US-09-974-546-2	Sequence 2, Appli
	34	20.2	49.3	642	21	US-10-489-864-2	Sequence 2, Appli
c	35	20.2	49.3	858	13	US-10-027-632-138797	Sequence 138797,
c	36	20.2	49.3	858	13	US-10-027-632-138798	Sequence 138798,
c	37	20.2	49.3	858	17	US-10-027-632-138797	Sequence 138797,
c	38	20.2	49.3	858	17	US-10-027-632-138798	Sequence 138798,
	39	20.2	49.3	990	18	US-10-425-114-19245	Sequence 19245, A
c	40	20.2	49.3	1047	18	US-10-425-114-14253	Sequence 14253, A
c	41	20.2	49.3	1176	20	US-10-425-115-117351	Sequence 117351,
	42	20.2	49.3	1455	9	US-09-938-842A-440	Sequence 440, App
	43	20.2	49.3	1455	11	US-09-938-842A-440	Sequence 440, App
c	44	20.2	49.3	1672	21	US-10-489-864-1	Sequence 1, Appli
	45	20.2	49.3	1911	20	US-10-411-910A-225	Sequence 225, App

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OM nucleic - nucleic search, using sw model

Run on: October 11, 2005, 06:09:25 ; Search time 11.2549 Seconds
(without alignments)
5960.722 Million cell updates/sec

Title: US-10-798-678-12
Perfect score: 41
Sequence: 1 atcatgcgcttcaccgactg.....gagaaagagcctctccgtcc 41

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				Description
	No.	Score	Match	Length	ID	ID	
	1	22.6	55.1	80858	4	US-09-949-016-12659	Sequence 12659, A
	2	22.6	55.1	80859	4	US-09-949-016-15715	Sequence 15715, A
	3	22	53.7	601	4	US-09-949-016-195479	Sequence 195479,
	4	22	53.7	601	4	US-09-949-016-195480	Sequence 195480,
c	5	22	53.7	112114	4	US-09-949-016-17292	Sequence 17292, A
c	6	22	53.7	154605	4	US-09-949-016-11894	Sequence 11894, A
c	7	20.4	49.8	192506	4	US-09-949-016-15830	Sequence 15830, A
c	8	20.2	49.3	614	2	US-08-692-787-2	Sequence 2, Appli
c	9	20.2	49.3	614	3	US-09-097-199-2	Sequence 2, Appli
c	10	20.2	49.3	1773	4	US-09-489-039A-241	Sequence 241, App
c	11	20	48.8	601	4	US-09-949-016-152018	Sequence 152018,

	12	20	48.8	601	4	US-09-949-016-168940	Sequence 168940,
c	13	20	48.8	1258	4	US-09-016-434-1294	Sequence 1294, Ap
c	14	20	48.8	1258	4	US-09-949-016-112	Sequence 112, App
c	15	20	48.8	1262	4	US-09-949-016-3837	Sequence 3837, Ap
	16	20	48.8	2938	3	US-09-072-917A-8	Sequence 8, Appli
	17	20	48.8	7353	4	US-09-949-016-14895	Sequence 14895, A
c	18	20	48.8	16198	4	US-09-949-016-11854	Sequence 11854, A
c	19	20	48.8	16198	4	US-09-949-016-15579	Sequence 15579, A
	20	20	48.8	39498	4	US-09-949-016-12410	Sequence 12410, A
	21	20	48.8	39498	4	US-09-949-016-16505	Sequence 16505, A
c	22	20	48.8	41393	4	US-09-949-016-16012	Sequence 16012, A
c	23	19.8	48.3	165	4	US-09-513-999C-24787	Sequence 24787, A
	24	19.8	48.3	360	4	US-09-621-976-2422	Sequence 2422, Ap
	25	19.8	48.3	3222	4	US-09-902-540-3000	Sequence 3000, Ap
c	26	19.8	48.3	13332	4	US-09-902-540-1047	Sequence 1047, Ap
c	27	19.8	48.3	57859	4	US-09-949-016-12334	Sequence 12334, A
c	28	19.8	48.3	57859	4	US-09-949-016-14657	Sequence 14657, A
c	29	19.8	48.3	57859	4	US-09-949-016-14658	Sequence 14658, A
	30	19.6	47.8	601	4	US-09-949-016-26911	Sequence 26911, A
	31	19.6	47.8	601	4	US-09-949-016-26912	Sequence 26912, A
	32	19.6	47.8	601	4	US-09-949-016-26913	Sequence 26913, A
	33	19.6	47.8	601	4	US-09-949-016-182952	Sequence 182952,
	34	19.6	47.8	601	4	US-09-949-016-182953	Sequence 182953,
	35	19.6	47.8	601	4	US-09-949-016-182954	Sequence 182954,
	36	19.6	47.8	771	4	US-09-489-039A-419	Sequence 419, App
c	37	19.6	47.8	972	4	US-09-583-110-1979	Sequence 1979, Ap
c	38	19.6	47.8	972	4	US-09-107-433-676	Sequence 676, App
	39	19.6	47.8	3332	3	US-09-448-806C-1	Sequence 1, Appli
	40	19.6	47.8	3401	4	US-09-555-554-3	Sequence 3, Appli
	41	19.6	47.8	3441	4	US-09-095-881-1	Sequence 1, Appli
	42	19.6	47.8	4108	3	US-08-981-729-8	Sequence 8, Appli
	43	19.6	47.8	4108	3	US-08-981-446B-1	Sequence 1, Appli
	44	19.6	47.8	4108	4	US-09-613-811-8	Sequence 8, Appli
c	45	19.6	47.8	7174	3	US-08-961-527-189	Sequence 189, App

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OM nucleic - nucleic search, using sw model

Run on: October 11, 2005, 06:09:23 ; Search time 36.4176 Seconds
(without alignments)
6664.609 Million cell updates/sec

Title: US-10-798-678-12
Perfect score: 41
Sequence: 1 atcatgcgcttcaccgactg.....gagaaagagcctctccgtcc 41

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	41	100.0	41	13	ADS13183	Ads13183 PCR prime
c 2	24	58.5	1115	13	ADS13173	Ads13173 Porcine c
3	22.8	55.6	110000	12	ADN46845_09	Continuation (10 o
c 4	22.8	55.6	110000	12	ADN47591_10	Continuation (11 o

c	5	22.8	55.6	110000	12	ADN47591_11	Continuation (12 o
	6	22.8	55.6	110000	12	ADN46123_09	Continuation (10 o
c	7	22.8	55.6	110000	12	ADN47209_10	Continuation (11 o
c	8	22.8	55.6	110000	12	ADN47209_11	Continuation (12 o
	9	22.8	55.6	110000	12	ADN46464_09	Continuation (10 o
c	10	22.8	55.6	110000	12	ADN47960_10	Continuation (11 o
c	11	22.8	55.6	110000	12	ADN47960_11	Continuation (12 o
	12	22.6	55.1	11987	4	AAL07284	Aal07284 Human rep
	13	22.6	55.1	11987	4	ABL98830	Ab198830 Human tes
c	14	21.6	52.7	504	12	ACH74832	Ach74832 Human gen
	15	21.2	51.7	7588	3	AAA54015	Aaa54015 6-Methyls
	16	21.2	51.7	9524	3	AAA54014	Aaa54014 6-Methyls
	17	21.2	51.7	110000	12	ADN46845_07	Continuation (8 of
c	18	21.2	51.7	110000	12	ADN47591_13	Continuation (14 o
	19	21.2	51.7	110000	12	ADN46123_07	Continuation (8 of
c	20	21.2	51.7	110000	12	ADN47209_13	Continuation (14 o
	21	21.2	51.7	110000	12	ADN46464_07	Continuation (8 of
c	22	21.2	51.7	110000	12	ADN47960_13	Continuation (14 o
c	23	20.8	50.7	3401	10	ADB68999	Adb68999 C. neofor
	24	20.6	50.2	462	4	ABL28135	Ab128135 Drosophil
	25	20.6	50.2	1365	4	ABL25753	Ab125753 Drosophil
c	26	20.6	50.2	3464	4	ABL25752	Ab125752 Drosophil
c	27	20.6	50.2	3759	4	ABL05751	Ab105751 Drosophil
	28	20.6	50.2	4510	4	ABL28134	Ab128134 Drosophil
c	29	20.6	50.2	6020	4	ABL05750	Ab105750 Drosophil
	30	20.6	50.2	147309	6	ABK49450	Abk49450 Human tra
	31	20.4	49.8	12210	4	AAK70458	Aak70458 Human imm
	32	20.4	49.8	12210	4	AAK78929	Aak78929 Human imm
	33	20.4	49.8	304905	11	ADP75180	Adp75180 Human End
	34	20.2	49.3	257	12	ADL83696	Adl83696 DNA up-re
	35	20.2	49.3	257	12	ADL83697	Adl83697 DNA up-re
	36	20.2	49.3	585	8	ABZ77656	Abz77656 Nucleotid
c	37	20.2	49.3	614	2	AAV16882	Aav16882 Human pro
c	38	20.2	49.3	614	2	AAX26017	Aax26017 Prostate
c	39	20.2	49.3	614	3	AAZ87502	Aaz87502 Prostate,
c	40	20.2	49.3	614	4	AAS03721	Aas03721 Biomarker
	41	20.2	49.3	642	8	ABZ77655	Abz77655 Nucleotid
	42	20.2	49.3	1455	6	ABZ12635	Abz12635 Arabidops
	43	20.2	49.3	1455	12	ADN72266	Adn72266 Thale cre
c	44	20.2	49.3	1672	8	ABZ77654	Abz77654 Nucleotid
c	45	20.2	49.3	1773	11	ACH94446	Ach94446 Klebsiell

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OM nucleic - nucleic search, using sw model

Run on: October 11, 2005, 06:09:23 ; Search time 196.934 Seconds
(without alignments)
10087.968 Million cell updates/sec

Title: US-10-798-678-12
Perfect score: 41
Sequence: 1 atcatgcgcttcaccgactg.....gagaaagagcctctccgtcc 41

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	26.2	63.9	148202	10	AL928553	AL928553 Mouse DNA
2	23.4	57.1	172901	2	AC151240	AC151240 Bos tauru
3	23.4	57.1	187455	2	AC150757	AC150757 Bos tauru

c	4	23	56.1	98914	2	AC114724_3	Continuation (4 of
	5	23	56.1	144077	10	AL844511	AL844511 Mouse DNA
	6	23	56.1	254538	2	AC097032	AC097032 Rattus no
	7	22.6	55.1	1026	14	AF013386	AF013386 Meaban vi
c	8	22.6	55.1	81255	2	AC017607	AC017607 Drosophil
	9	22.6	55.1	110000	3	AE003597_2	Continuation (3 of
c	10	22.6	55.1	166036	2	AC145332	AC145332 Felis cat
	11	22.6	55.1	169841	3	AC009366	AC009366 Drosophil
	12	22.6	55.1	179613	3	AC023676	AC023676 Drosophil
c	13	22.6	55.1	183334	9	AC020558	AC020558 Homo sapi
	14	22.6	55.1	183427	2	AC090608	AC090608 Homo sapi
c	15	22.6	55.1	240797	2	AC099234	AC099234 Rattus no
	16	22.6	55.1	244566	10	AC126807	AC126807 Mus muscu
	17	22.4	54.6	129120	9	HS187B23	AL031280 Human DNA
	18	22.4	54.6	177562	9	HS269M15	AL021395 Human DNA
c	19	22.4	54.6	213240	2	AC147849	AC147849 Otolemur
c	20	22.4	54.6	225152	10	AC132454	AC132454 Mus muscu
c	21	22.4	54.6	235575	2	AC120088	AC120088 Rattus no
	22	22.4	54.6	285107	2	AC103104	AC103104 Rattus no
c	23	22.2	54.1	163351	10	AL928958	AL928958 Mouse DNA
c	24	22.2	54.1	196261	2	AC149008	AC149008 Otolemur
	25	22.2	54.1	224385	2	AC132124	AC132124 Mus muscu
c	26	22	53.7	800	8	AF486634	AF486634 Triticum
c	27	22	53.7	865	3	AF172720	AF172720 Strongylo
c	28	22	53.7	2230	1	AF228582	AF228582 Actinomyc
	29	22	53.7	2709	14	AF310937	AF310937 Powassan
	30	22	53.7	2709	14	AF310939	AF310939 Powassan
	31	22	53.7	2709	14	AF310940	AF310940 Powassan
	32	22	53.7	2709	14	AF310941	AF310941 Powassan
c	33	22	53.7	3063	9	HSM801423	AL133573 Homo sapi
	34	22	53.7	10839	14	PWARPT	L06436 Powassan vi
c	35	22	53.7	148362	8	AP004361	AP004361 Oryza sat
c	36	22	53.7	156300	9	AC026620	AC026620 Homo sapi
	37	22	53.7	157026	2	AC120256	AC120256 Rattus no
	38	22	53.7	166811	2	AC018941	AC018941 Homo sapi
c	39	22	53.7	184841	2	AC129486	AC129486 Homo sapi
	40	22	53.7	186152	2	AC130358	AC130358 Homo sapi
	41	22	53.7	190632	10	AC110622	AC110622 Mus muscu
c	42	22	53.7	192583	2	AC015941	AC015941 Homo sapi
c	43	22	53.7	215441	9	AC005736	AC005736 Homo sapi
	44	22	53.7	236874	2	AC115267	AC115267 Rattus no
	45	22	53.7	250517	2	AC094734	AC094734 Rattus no

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OM nucleic - nucleic search, using sw model

Run on: October 11, 2005, 06:09:23 ; Search time 310.207 Seconds
(without alignments)
5030.955 Million cell updates/sec

Title: US-10-798-678-11
Perfect score: 41
Sequence: 1 cgagggctgttaaaggccaa.....gctcctttctccaggacac 41

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	%		DB	ID	Description
			Query	Match Length			
c	1	24.8	60.5	821	5	BU599511	BU599511 AGENCOURT
c	2	23.6	57.6	603	1	AJ656330	AJ656330 AJ656330
	3	23.6	57.6	645	8	AZ998017	AZ998017 2M0284F17
c	4	23.4	57.1	375	5	BP629928	BP629928 BP629928
c	5	23.4	57.1	414	1	AA443873	AA443873 zw92g11.r
	6	23.2	56.6	159	6	CA570344	CA570344 K0505C12-
c	7	23.2	56.6	318	7	CV091762	CV091762 Mdfrt3082
	8	23.2	56.6	376	7	CN662923	CN662923 A0741H04-

	9	23.2	56.6	463	6	CA572463	CA572463	K0535E11-
	10	23.2	56.6	477	6	CA572096	CA572096	K0529B08-
	11	23.2	56.6	491	5	BQ562329	BQ562329	H4075D03-
	12	23.2	56.6	519	6	CA570694	CA570694	K0509F09-
c	13	23.2	56.6	765	9	CC582730	CC582730	CH240_378
	14	23.2	56.6	1930	2	BF535182	BF535182	602054246
c	15	23	56.1	618	9	CE313667	CE313667	tigr-gss-
c	16	23	56.1	743	5	BX873313	BX873313	BX873313
	17	23	56.1	774	8	BH246921	BH246921	BOGAJ70TF
	18	22.8	55.6	105	9	CG531542	CG531542	OST114379
c	19	22.6	55.1	333	7	F10375	F10375	HSC3EC012 n
	20	22.6	55.1	374	4	BM429790	BM429790	1Duo21D12
	21	22.6	55.1	462	2	AW430552	AW430552	70223 MAR
c	22	22.6	55.1	927	5	BQ431079	BQ431079	AGENCOURT
	23	22.6	55.1	1159	9	CL471466	CL471466	SAIL_160_
c	24	22.4	54.6	262	1	AA047755	AA047755	zf14h03.r
c	25	22.4	54.6	276	7	T80897	T80897	yd25e04.r1
	26	22.4	54.6	439	7	CK382707	CK382707	lag42c12.
	27	22.4	54.6	590	9	BX957697	BX957697	Reverse s
	28	22.4	54.6	637	2	BB664832	BB664832	BB664832
	29	22.4	54.6	919	2	BF179486	BF179486	601807361
c	30	22.2	54.1	370	1	AV657765	AV657765	AV657765
c	31	22.2	54.1	571	9	CR810577	CR810577	GR0AAA34A
	32	22.2	54.1	586	7	CR429620	CR429620	CR429620
c	33	22.2	54.1	709	4	BM728969	BM728969	UI-E-EO1-
c	34	22.2	54.1	1478	4	BI333843	BI333843	602999359
c	35	22	53.7	386	1	AJ654090	AJ654090	AJ654090
	36	22	53.7	567	4	BI398719	BI398719	MI-P-AY1-
	37	22	53.7	578	1	AI994421	AI994421	701496318
	38	22	53.7	587	6	C86905	C86905	C86905 Mous
	39	22	53.7	600	5	BU923713	BU923713	7064-63 M
c	40	22	53.7	636	5	BX668147	BX668147	BX668147
c	41	22	53.7	646	6	CA589187	CA589187	hab54h11.
	42	22	53.7	646	6	CB475213	CB475213	jns104_F0
	43	22	53.7	651	6	CB479636	CB479636	jns52_H07
	44	22	53.7	674	7	CF362814	CF362814	830609 MA
	45	22	53.7	676	7	CF362793	CF362793	830584 MA

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OM nucleic - nucleic search, using sw model

Run on: October 11, 2005, 06:09:25 ; Search time 118.069 Seconds
(without alignments)
2418.567 Million cell updates/sec

Title: US-10-798-678-11
Perfect score: 41
Sequence: 1 cgagggctgttaaaggccaa.....gctcctttctccaggacac 41

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 8443130 seqs, 3482420727 residues

Total number of hits satisfying chosen parameters: 16886260

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:*
- 22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match Length	DB	ID	Description	
	1	41	100.0	41	20	US-10-798-678-11	Sequence 11, Appl
	2	24	58.5	454	20	US-10-653-047-656	Sequence 656, App
	3	24	58.5	1578	22	US-10-450-763-5698	Sequence 5698, Ap
c	4	23.4	57.1	414	20	US-10-723-860-2943	Sequence 2943, Ap
	5	23	56.1	600	22	US-10-972-079-33077	Sequence 33077, A
	6	23	56.1	600	22	US-10-972-079-33078	Sequence 33078, A
	7	23	56.1	600	22	US-10-972-079-33079	Sequence 33079, A
	8	23	56.1	326014	9	US-09-731-231A-3	Sequence 3, Appli
	9	23	56.1	326014	19	US-10-751-985-3	Sequence 3, Appli
	10	22.8	55.6	105	9	US-09-728-444-576	Sequence 576, App
	11	22.8	55.6	350	20	US-10-425-115-126127	Sequence 126127,
	12	22.6	55.1	92292	20	US-10-719-993-6838	Sequence 6838, Ap
	13	22.6	55.1	96599	17	US-10-085-117-100	Sequence 100, App
	14	22	53.7	612	19	US-10-767-701-6927	Sequence 6927, Ap
	15	21.8	53.2	212	16	US-10-029-386-15591	Sequence 15591, A
	16	21.8	53.2	535	16	US-10-029-386-1891	Sequence 1891, Ap
c	17	21.8	53.2	1619	22	US-10-450-763-23996	Sequence 23996, A
c	18	21.8	53.2	2274	22	US-10-450-763-23366	Sequence 23366, A
c	19	21.8	53.2	2607	22	US-10-450-763-23367	Sequence 23367, A
	20	21.8	53.2	10180	21	US-10-893-671-66	Sequence 66, Appl
c	21	21.6	52.7	663	22	US-10-450-763-4144	Sequence 4144, Ap
c	22	21.6	52.7	1067	16	US-10-094-097B-254	Sequence 254, App
c	23	21.6	52.7	133100	22	US-10-723-681-4	Sequence 4, Appli
c	24	21.6	52.7	744802	17	US-10-292-798-1369	Sequence 1369, Ap
c	25	21.4	52.2	323	20	US-10-425-115-66750	Sequence 66750, A
	26	21.4	52.2	1005	22	US-10-450-763-7354	Sequence 7354, Ap
	27	21.4	52.2	414295	20	US-10-719-993-6876	Sequence 6876, Ap
	28	21.2	51.7	300	21	US-10-696-639-580	Sequence 580, App
c	29	21.2	51.7	22260	17	US-10-085-117-298	Sequence 298, App
c	30	21.2	51.7	143306	9	US-09-729-920-3	Sequence 3, Appli
c	31	21.2	51.7	143306	20	US-10-887-932-3	Sequence 3, Appli
c	32	21	51.2	463	20	US-10-425-115-76673	Sequence 76673, A
	33	21	51.2	681	13	US-10-027-632-38616	Sequence 38616, A
	34	21	51.2	681	13	US-10-027-632-38617	Sequence 38617, A
	35	21	51.2	681	17	US-10-027-632-38616	Sequence 38616, A
	36	21	51.2	681	17	US-10-027-632-38617	Sequence 38617, A
c	37	21	51.2	1095	13	US-10-027-632-81415	Sequence 81415, A
c	38	21	51.2	1095	13	US-10-027-632-81416	Sequence 81416, A
c	39	21	51.2	1095	17	US-10-027-632-81415	Sequence 81415, A
c	40	21	51.2	1095	17	US-10-027-632-81416	Sequence 81416, A
	41	20.8	50.7	455	13	US-10-027-632-50765	Sequence 50765, A
	42	20.8	50.7	455	13	US-10-027-632-317969	Sequence 317969,
	43	20.8	50.7	455	13	US-10-027-632-317970	Sequence 317970,
	44	20.8	50.7	455	17	US-10-027-632-50765	Sequence 50765, A
	45	20.8	50.7	455	17	US-10-027-632-317969	Sequence 317969,

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OM nucleic - nucleic search, using sw model

Run on: October 11, 2005, 06:09:25 ; Search time 11.2549 Seconds
(without alignments)
5960.722 Million cell updates/sec

Title: US-10-798-678-11
Perfect score: 41
Sequence: 1 cgagggtgttaaaggccaa.....gctcctttctccaggacac 41

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				ID	Description
	No.	Score	Match	Length	DB	Query		
	1	22.6	55.1	83851	4	US-09-949-016-13847		Sequence 13847, A
	2	21.2	51.7	601	4	US-09-949-016-79200		Sequence 79200, A
c	3	21.2	51.7	146095	4	US-09-949-016-12872		Sequence 12872, A
c	4	21.2	51.7	146104	4	US-09-949-016-13239		Sequence 13239, A
	5	21.2	51.7	784019	4	US-09-949-016-14033		Sequence 14033, A
	6	21.2	51.7	828152	4	US-09-949-016-12777		Sequence 12777, A
c	7	21	51.2	601	4	US-09-949-016-175322		Sequence 175322, A
	8	21	51.2	22988	4	US-09-949-016-16721		Sequence 16721, A
	9	20.8	50.7	147	4	US-09-270-767-5464		Sequence 5464, Ap
	10	20.8	50.7	147	4	US-09-270-767-20746		Sequence 20746, A
	11	20.8	50.7	1826	4	US-09-799-451-284		Sequence 284, App

	12	20.8	50.7	3978	3	US-08-726-214-1	Sequence 1, Appli
c	13	20.8	50.7	312470	4	US-09-949-016-14043	Sequence 14043, A
c	14	20.8	50.7	336024	4	US-09-949-016-12373	Sequence 12373, A
c	15	20.6	50.2	13782	4	US-09-949-016-14992	Sequence 14992, A
c	16	20.4	49.8	107	2	US-08-476-176B-28	Sequence 28, Appl
c	17	20.4	49.8	107	3	US-08-127-721A-28	Sequence 28, Appl
c	18	20.4	49.8	107	3	US-08-485-246A-28	Sequence 28, Appl
	19	20.4	49.8	467	2	US-08-476-176B-15	Sequence 15, Appl
	20	20.4	49.8	467	3	US-08-127-721A-15	Sequence 15, Appl
	21	20.4	49.8	467	3	US-08-485-246A-15	Sequence 15, Appl
	22	20.4	49.8	468	2	US-08-476-176B-11	Sequence 11, Appl
	23	20.4	49.8	468	3	US-08-127-721A-11	Sequence 11, Appl
	24	20.4	49.8	468	3	US-08-485-246A-11	Sequence 11, Appl
c	25	20	48.8	601	4	US-09-949-016-53351	Sequence 53351, A
	26	20	48.8	1249	2	US-08-933-750C-62	Sequence 62, Appl
	27	20	48.8	1249	3	US-09-234-613-62	Sequence 62, Appl
c	28	20	48.8	1622	1	US-08-631-200-13	Sequence 13, Appl
c	29	20	48.8	1622	1	US-08-829-553-13	Sequence 13, Appl
c	30	20	48.8	1622	2	US-08-922-267A-13	Sequence 13, Appl
c	31	20	48.8	1622	2	US-08-936-707A-13	Sequence 13, Appl
c	32	20	48.8	1622	2	US-08-936-706A-13	Sequence 13, Appl
c	33	20	48.8	1622	3	US-09-248-203-13	Sequence 13, Appl
c	34	20	48.8	1622	3	US-09-406-071-13	Sequence 13, Appl
c	35	20	48.8	1622	4	US-09-814-986-13	Sequence 13, Appl
c	36	20	48.8	5085	4	US-09-949-016-5856	Sequence 5856, Ap
c	37	20	48.8	13187	4	US-09-949-016-5062	Sequence 5062, Ap
c	38	20	48.8	14770	4	US-09-220-132-30	Sequence 30, Appl
c	39	20	48.8	14770	4	US-09-949-016-1107	Sequence 1107, Ap
c	40	20	48.8	50269	4	US-09-949-016-17598	Sequence 17598, A
	41	20	48.8	139936	4	US-09-949-016-11782	Sequence 11782, A
	42	20	48.8	139952	4	US-09-949-016-13280	Sequence 13280, A
c	43	20	48.8	176006	4	US-09-949-016-16804	Sequence 16804, A
c	44	20	48.8	253375	4	US-09-949-016-12849	Sequence 12849, A
	45	19.8	48.3	460	4	US-09-621-976-11014	Sequence 11014, A

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OM nucleic - nucleic search, using sw model

Run on: October 11, 2005, 06:09:23 ; Search time 36.4176 Seconds
(without alignments)
6664.609 Million cell updates/sec

Title: US-10-798-678-11
Perfect score: 41
Sequence: 1 cgagggctgttaaaggccaa.....gctcctttctccaggacac 41

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	41	100.0	41	13	ADS13182
2	24	58.5	454	3	AAF08133
3	24	58.5	1578	5	AAS69894
c 4	23.4	57.1	414	12	ADQ20123

Ads13182 PCR prime
Aaf08133 Fusarium
Aas69894 DNA encod
Adq20123 Human sof

	5	23.2	56.6	137454	12	ADQ97388	Adq97388 Mouse can
	6	23	56.1	326014	6	ABK89296	Abk89296 Human gen
	7	23	56.1	326014	12	ADQ94981	Adq94981 Human kin
	8	22.8	55.6	105	8	ABX91232	Abx91232 Murine ge
c	9	22	53.7	61557	4	AAS59521	Aas59521 Propionib
c	10	22	53.7	61557	8	ACF64450	Acf64450 Propionib
	11	21.8	53.2	212	12	ACH82396	Ach82396 Human gen
	12	21.8	53.2	535	12	ACH68696	Ach68696 Human gen
c	13	21.8	53.2	1619	5	AAS88192	Aas88192 DNA encod
c	14	21.8	53.2	2274	5	AAS87562	Aas87562 DNA encod
c	15	21.8	53.2	2607	5	AAS87563	Aas87563 DNA encod
	16	21.8	53.2	10180	4	AAS46263	Aas46263 DNA encod
c	17	21.6	52.7	663	5	AAS68340	Aas68340 DNA encod
c	18	21.6	52.7	133100	12	ADP45594	Adp45594 Human NUM
c	19	21.6	52.7	349981	10	ADC87619	Adc87619 Human GPC
	20	21.4	52.2	951	6	ABQ80804	Abq80804 Nucleotid
	21	21.4	52.2	1005	5	AAS71550	Aas71550 DNA encod
	22	21.4	52.2	1127	3	AAC51253	Aac51253 Arabidops
	23	21.4	52.2	1129	3	AAC41095	Aac41095 Arabidops
	24	21.2	51.7	378	4	AAK76349	Aak76349 Human imm
	25	21.2	51.7	381	4	AAK59847	Aak59847 Human imm
	26	21.2	51.7	1540	6	AAS16260	Aas16260 cDNA enco
c	27	21.2	51.7	143306	6	ABK49586	Abk49586 Human tra
	28	20.8	50.7	549	9	ACC73130	Acc73130 Cat flea
	29	20.8	50.7	549	12	ADL09775	Adl09775 Cat flea
c	30	20.8	50.7	568	12	ACH68035	Ach68035 Human gen
	31	20.8	50.7	1020	13	ADT48187	Adt48187 Bacterial
	32	20.8	50.7	1826	6	ABZ11402	Abz11402 Human pol
	33	20.8	50.7	1826	12	ADM43920	Adm43920 Novel hum
c	34	20.8	50.7	2302	13	ADS09995	Ads09995 Human the
	35	20.8	50.7	3978	3	AAA53918	Aaa53918 Adenylyl
	36	20.8	50.7	4876	13	ADR07200	Adr07200 Full leng
	37	20.8	50.7	8172	13	ADR84282	Adr84282 Aspergill
	38	20.8	50.7	113585	12	ADJ19197	Adj19197 Human int
c	39	20.6	50.2	376	6	ABL77191	Abl77191 Human ova
c	40	20.6	50.2	110000	12	ADN46845_13	Continuation (14 o
	41	20.6	50.2	110000	12	ADN47591_07	Continuation (8 of
c	42	20.6	50.2	110000	12	ADN46123_13	Continuation (14 o
	43	20.6	50.2	110000	12	ADN47209_07	Continuation (8 of
c	44	20.6	50.2	110000	12	ADN46464_13	Continuation (14 o
	45	20.6	50.2	110000	12	ADN47960_07	Continuation (8 of

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OM nucleic - nucleic search, using sw model

Run on: October 11, 2005, 06:09:23 ; Search time 196.934 Seconds
(without alignments)
10087.968 Million cell updates/sec

Title: US-10-798-678-11
Perfect score: 41
Sequence: 1 cgagggctgttaaaggccaa.....gctcctttctccagggacac 41

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	24.6	60.0	152881	10	AC124353	AC124353 Mus muscu
c	2	24.6	60.0	167753	2	AC126039	AC126039 Mus muscu
	3	24.6	60.0	184420	2	AC118373	AC118373 Rattus no

	4	24.4	59.5	189867	2	AC128902	AC128902 Rattus no
	5	24.4	59.5	208281	2	AC106260	AC106260 Rattus no
	6	24.4	59.5	211621	2	AC127128	AC127128 Rattus no
C	7	24	58.5	164223	2	AC127176	AC127176 Rattus no
C	8	24	58.5	214415	9	AC010674	AC010674 Homo sapi
	9	23.8	58.0	216161	9	AC024558	AC024558 Homo sapi
	10	23.6	57.6	758	11	BV017381	BV017381 S212P6043
C	11	23.6	57.6	240053	2	AC113002	AC113002 Mus muscu
C	12	23.4	57.1	169541	9	AL136178	AL136178 Human DNA
C	13	23.4	57.1	171460	9	AC069213	AC069213 Homo sapi
C	14	23.4	57.1	186496	2	AC020573	AC020573 Homo sapi
	15	23.4	57.1	199504	2	AC121022	AC121022 Rattus no
	16	23.4	57.1	243134	2	AC135525	AC135525 Rattus no
	17	23.2	56.6	80460	10	AL513014	AL513014 Mouse DNA
C	18	23.2	56.6	110000	2	AC107144_3	Continuation (4 of
	19	23.2	56.6	161204	9	CNS01RI1	AL162811 Human chr
	20	23.2	56.6	194405	2	AC021122	AC021122 Homo sapi
	21	23.2	56.6	220154	2	AC117695	AC117695 Mus muscu
	22	23.2	56.6	230337	2	AC140776	AC140776 Mus muscu
C	23	23.2	56.6	239126	2	AC098416	AC098416 Rattus no
C	24	23.2	56.6	265998	2	AC127143	AC127143 Rattus no
C	25	23.2	56.6	292664	2	AC103298	AC103298 Rattus no
	26	23	56.1	2825	3	THESPAGI	M63017 Theileria a
	27	23	56.1	70231	5	AC092870	AC092870 Takifugu
	28	23	56.1	90695	9	HS257I9	AL031773 Human DNA
	29	23	56.1	97166	2	AC098643	AC098643 Takifugu
	30	23	56.1	97681	9	AL138931	AL138931 Human DNA
C	31	23	56.1	111568	9	AC083908	AC083908 Homo sapi
	32	23	56.1	153694	2	AL355359	AL355359 Homo sapi
C	33	23	56.1	175923	2	AC064839	AC064839 Homo sapi
	34	23	56.1	240238	2	AC095867	AC095867 Rattus no
	35	23	56.1	243639	2	AC109943	AC109943 Rattus no
	36	23	56.1	255354	2	AC126830	AC126830 Rattus no
C	37	23	56.1	263051	2	CR450811	CR450811 Danio rer
	38	23	56.1	299633	2	AC103160	AC103160 Rattus no
C	39	23	56.1	300626	2	AC095973	AC095973 Rattus no
	40	22.8	55.6	183088	9	AC007600	AC007600 Homo sapi
	41	22.8	55.6	194198	2	AC013298	AC013298 Homo sapi
C	42	22.8	55.6	194632	9	AC096996	AC096996 Homo sapi
	43	22.8	55.6	203558	10	AL670464	AL670464 Mouse DNA
C	44	22.6	55.1	333	11	G21690	G21690 human STS W
C	45	22.6	55.1	59094	9	AC109780	AC109780 Homo sapi